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(54) **Identification of tumor-associated markers for diagnosis and therapy**

(57) The invention relates to genetic products the ex-
pression of which is associated with cancer diseases.
The invention also relates to the therapy and diagnosis

of diseases in which the genetic products are expressed
or aberrantly expressed, in particular cancer diseases.

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Description

[0001] The invention relates to nucleic acids and encoded polypeptides which are expressed in cancers. The invention also relates to agents which bind the polypeptides. The nucleic acids, polypeptides coded for by such nucleic acids and peptides derived therefrom, as well as related antibodies and cytolytic T lymphocytes, are useful, inter alia, in diagnostic and therapeutic contexts.

[0002] Despite interdisciplinary approaches and exhaustive use of classical therapeutic procedures, cancers are still among the leading causes of death.

[0003] More recent therapeutic concepts in cancer therapy aim at incorporating the patient's immune system into the overall therapeutic concept by using recombinant tumor vaccines and other specific measures such as antibody therapy. A prerequisite for the success of such a strategy is the recognition of tumor-specific or tumor-associated antigens or epitopes by the patient's immune system whose effector functions are to be interventionally enhanced.

[0004] Tumor cells biologically differ substantially from their nonmalignant cells of origin. These differences are due to genetic alterations acquired during tumor development and result, inter alia, also in the formation of qualitatively or quantitatively altered molecular structures in the cancer cells. Tumor-associated structures of this kind which are recognized by the specific immune system of the tumor-harboring host are referred to as tumor-associated antigens.

[0005] The specific recognition of tumor-associated antigens involves cellular and humoral mechanisms which are two functionally interconnected units: CD4⁺ and CD8⁺ T lymphocytes recognize the processed antigens presented on the molecules of the MHC (major histocompatibility complex) classes II and I, respectively, while B lymphocytes produce circulating antibody molecules which bind directly to unprocessed antigens. The potential clinical-therapeutical importance of tumor-associated antigens results from the fact that the recognition of antigens on neoplastic cells by the immune system leads to the initiation of cytotoxic effector mechanisms and, in the presence of T helper cells, can cause elimination of the cancer cells (Pardoll, Nat. Med. 4:525-31, 1998).

[0006] Antibody based cancer therapies have been successfully introduced into the clinic and have emerged as the most promising therapeutics in oncology over the last decade. Eight antibodies have been approved for treatment of neoplastic diseases, most of them, however in lymphoma and leukemia (Adams GP, Weiner LM, Nat Biotechnol 23: 1147-57, 2005).

[0007] One of the challenges to be mastered for the advent of the next generation of upgraded antibody-based cancer therapeutics is the selection of appropriate target molecules, which is the key for a favorable toxicity/efficacy profile.

[0008] The search for genes tightly silenced in the vast majority of healthy tissues moves into the focus of attention the intriguing observation that genes of the gametogenic and/or trophoblastic lineage are frequently ectopically activated and robustly expressed in human cancer. Based on phenotypical similarities between germ cells, pregnancy trophoblast and cancer cells, John Beard proposed as much as 100 years ago a "trophoblastic theory of cancer" (Beard J, Lancet 1:1758-63, 1902; Gurchot C, Oncology 31:310-3, 1975). The discovery of the sporadic production of chorionic gonadotropin, alpha-fetoprotein, CEA and other trophoblastic hormones by cancer cells provided the first molecules shared between neoplastic and trophoblastic cells (Acevedo HF et al., Cancer 76:1467-75, 1995; Dirnhofer S et al., Hum Pathol 29:377-82, 1998; Gurchot C, Oncology 31:310-3, 1975; Iles RK, Chard T, J Urol 145:453-8, 1991; Laurence DJ, Neville AM, Br J Cancer 26:335-55, 1972). The concept was reignited by the inauguration of the steadily growing so-called cancer/germline (CG) class of genes, which represents more than 100 members, each expressed in a variety of tumor types. The observation that entire trophoblastic and gametogenic programs escape transcriptional silencing and are ectopically activated in cancer cells (Koslowski M et al., Cancer Res 64:5988-93, 2004; Simpson AJ et al., Nat Rev Cancer 5:615-25, 2005) indicates that within this class of genes with exquisitely selective tissue distribution, appropriate targets for mAb therapy may be found.

[0009] It was the object of the present invention to provide target structures for a diagnosis and therapy of cancers.

[0010] This object is achieved by the subject matter of the claims.

[0011] According to the invention, placenta-specific genes are identified which are selectively or aberrantly expressed in tumor cells and thus, provide target structures for therapeutic and diagnostic approaches.

[0012] The nucleic acids identified according to the invention to be selectively or aberrantly expressed in tumor cells are selected from the group consisting of (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-540, 541, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624 of the sequence listing, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c). These nucleic acids are also termed "tumor-associated nucleic acids" herein.

[0013] In another aspect, the invention relates to antigens encoded by the tumor-associated nucleic acids identified according to the invention. Accordingly, the tumor-associated antigens identified according to the invention have an amino acid sequence encoded by a nucleic acid which is selected from the group consisting of (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-540, 541, 545, 549, 553, 557,

560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624 of the sequence listing, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c). In a preferred embodiment, the tumor-associated antigens identified according to the invention comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 542, 546, 550, 554, 567, 571, 584, 588, 592, 596, 603, 607, 614, 621, and 625 of the sequence listing, a part or derivative thereof.

[0014] If according to the invention reference is made to nucleic acids comprising certain nucleic acid sequences or tumor-associated antigens comprising certain amino acid sequences this also includes embodiments wherein the nucleic acids or tumor-associated antigens consist of these certain nucleic acid sequences or amino acid sequences, respectively.

[0015] The present invention generally relates to the use of tumor-associated nucleic acids and tumor-associated antigens identified according to the invention or of parts or derivatives thereof, of nucleic acids directed against said tumor-associated nucleic acids, of antibodies or T cells directed against the tumor-associated antigens identified according to the invention or parts or derivatives thereof and/or of host cells expressing the tumor-associated antigens identified according to the invention or parts or derivatives thereof for therapy, prophylaxis, diagnosis and/or monitoring of neoplastic diseases.

[0016] This may also involve the use of a combination of two or more of these nucleic acids, antigens, antibodies, T cells and/or host cells.

[0017] In those embodiments of the invention relating to the use of antibodies directed against the tumor-associated antigens identified according to the invention or parts or derivatives thereof also T cell receptors directed against the tumor-associated antigens identified according to the invention or parts or derivatives thereof, optionally in a complex with MHC molecules, may be used.

[0018] Especially suitable for therapy, prophylaxis, diagnosis and/or monitoring is a part of the tumor-associated antigens identified according to the invention which corresponds to the non-transmembrane portion, in particular the extracellular portion of the tumor-associated antigens or is comprised thereof. Therefore, according to the invention, a part of the tumor-associated antigens identified according to the invention which corresponds to the non-transmembrane portion, in particular the extracellular portion of the tumor-associated antigens or is comprised thereof, or a corresponding part of the nucleic acids coding for the tumor-associated antigens identified according to the invention is preferred for therapy, prophylaxis, diagnosis and/or monitoring. Similarly the use of antibodies is preferred which are directed against a part of the tumor-associated antigens identified according to the invention which corresponds to the non-transmembrane portion, in particular the extracellular portion of the tumor-associated antigens or is comprised thereof.

[0019] Preferred diseases for a therapy, prophylaxis, diagnosis and/or monitoring are those in which one or more of the tumor-associated nucleic acids identified according to the invention are selectively expressed or abnormally expressed. Particularly preferred diseases for a therapy, prophylaxis, diagnosis and/or monitoring are those in which one or more of the tumor-associated nucleic acids identified according to the invention and/or one or more of the tumor-associated antigens encoded thereby are selectively expressed or abnormally expressed.

[0020] In one aspect, the invention relates to a pharmaceutical composition comprising an agent which recognizes a tumor-associated antigen identified according to the invention or a nucleic acid coding for the tumor-associated antigen and which is preferably selective for cells which have expression or abnormal expression of a tumor-associated antigen identified according to the invention.

[0021] In a further aspect, the invention relates to a pharmaceutical composition comprising an agent which (I) inhibits expression or activity of a tumor-associated antigen identified according to the invention, and/or (II) has tumor-inhibiting or tumor-destroying activity and is selective for cells expressing or abnormally expressing a tumor-associated antigen identified according to the invention, and/or (III) when administered, selectively increases the amount of complexes between an MHC molecule and a tumor-associated antigen identified according to the invention or a part thereof, such as a peptide epitope. In particular embodiments, said agent may cause induction of cell death, reduction in cell growth, damage to the cell membrane or secretion of cytokines and preferably have a tumor-inhibiting activity.

[0022] In one embodiment, the agent is an antisense nucleic acid which hybridizes selectively with the nucleic acid coding for the tumor-associated antigen. In a further embodiment, the agent is a siRNA preferably comprising a sense RNA strand and an antisense RNA strand, wherein the sense and antisense RNA strands form an RNA duplex, and wherein the sense RNA strand comprises a nucleotide sequence substantially identical to a target sequence of about 19 to about 25 contiguous nucleotides in a nucleic acid coding for the tumor-associated antigen, preferably mRNA coding for the tumor-associated antigen. In a further embodiment, the agent is an antibody which binds selectively to the tumor-associated antigen, in particular a complement-activated or toxin conjugated antibody which binds selectively to the tumor-associated antigen. In a preferred embodiment, the antibody which binds selectively to the tumor-associated antigen is coupled to a therapeutically useful substance and/or recruits natural or artificial effector mechanisms to said cell expressing or abnormally expressing said tumor-associated antigen. In a further embodiment, the agent is a cytotoxic

T lymphocyte which recognizes the tumor-associated antigen or a part thereof bound by an MHC molecule on a cell and lyses the cells labeled in this way. In a further embodiment, the agent is a T helper lymphocyte which recognizes the tumor-associated antigen or a part thereof bound by an MHC molecule on a cell and enhances effector functions of other cells specifically recognizing said tumor-associated antigen or a part thereof.

[0023] In a further embodiment, the agent comprises two or more agents which each recognize different tumor-associated antigens or different nucleic acids coding for tumor-associated antigens and/or inhibit expression or activity of different tumor-associated antigens, and/or have tumor-inhibiting or tumor-destroying activity and are selective for cells expressing or abnormally expressing different tumor-associated antigens, and/or when administered, selectively increase the amount of complexes between MHC molecules and different tumor-associated antigens or parts thereof, wherein at least one of said different tumor-associated antigens is a tumor-associated antigen identified according to the invention.

[0024] Preferably, a tumor-associated antigen selectively limited to tumors serves as a label for recruiting effector mechanisms to this specific location. In this aspect, the invention includes embodiments wherein the agent itself does not have an ability to inhibit activity of a tumor-associated antigen or a tumor-inhibiting or tumor-destroying activity but mediates such effect, in particular by recruiting effector mechanisms, in particular those having cell damaging potential, to a specific location, in particular a tumor or tumor cells.

[0025] Preferably, said cells expressing or abnormally expressing a tumor-associated antigen identified according to the invention are non-placenta cells.

[0026] The activity of a tumor-associated antigen identified according to the invention can be any activity of a protein or a peptide. In one embodiment this activity is an enzymatic activity.

[0027] According to the invention the phrase "inhibit expression or activity" includes a complete or essentially complete inhibition of expression or activity and a reduction in expression or activity.

[0028] The agent which, when administered, selectively increases the amount of complexes between an MHC molecule and a tumor-associated antigen identified according to the invention or a part thereof comprises one or more components selected from the group consisting of (i) the tumor-associated antigen or a part thereof, (ii) a nucleic acid which codes for said tumor-associated antigen or a part thereof, (iii) a host cell which expresses said tumor-associated antigen or a part thereof, and (iv) isolated complexes between peptide epitopes from said tumor-associated antigen and an MHC molecule.

[0029] The invention furthermore relates to a pharmaceutical composition which comprises one or more components selected from the group consisting of (i) a tumor-associated antigen identified according to the invention or a part thereof, (ii) a nucleic acid which codes for a tumor-associated antigen identified according to the invention or a part thereof, (iii) an antibody which binds to a tumor-associated antigen identified according to the invention or to a part thereof, (iv) an antisense nucleic acid which hybridizes specifically with a tumor-associated nucleic acid identified according to the invention / a nucleic acid coding for a tumor-associated antigen identified according to the invention, (v) an siRNA directed against a tumor-associated nucleic acid identified according to the invention / a nucleic acid coding for a tumor-associated antigen identified according to the invention, (vi) a host cell which expresses a tumor-associated antigen identified according to the invention or a part thereof, and (vii) isolated complexes between a tumor-associated antigen identified according to the invention or a part thereof and an MHC molecule.

[0030] In one embodiment, a nucleic acid coding for a tumor-associated antigen identified according to the invention or a part thereof is present in the pharmaceutical composition in an expression vector and functionally linked to a promoter. In a further embodiment, a nucleic acid coding for a tumor-associated antigen identified according to the invention or a part thereof is present in the pharmaceutical composition in a virus as further described below.

[0031] A host cell present in a pharmaceutical composition of the invention may secrete the tumor-associated antigen or the part thereof, may express it on the surface and preferably may additionally express an MHC molecule which binds to said tumor-associated antigen or said part thereof. In one embodiment, the host cell expresses the MHC molecule endogenously. In a further embodiment, the host cell expresses the MHC molecule and/or the tumor-associated antigen or the part thereof in a recombinant manner. The host cell is preferably nonproliferative. In a preferred embodiment, the host cell is an antigen-presenting cell, in particular a dendritic cell, a monocyte or a macrophage.

[0032] In a further embodiment, an antibody present in a pharmaceutical composition of the invention is a monoclonal antibody. In further embodiments, the antibody is a chimeric or humanized antibody, a fragment of an antibody or a synthetic antibody. The antibody may be coupled to a therapeutically or diagnostically useful agent also termed therapeutic or diagnostic agent herein.

[0033] An antisense nucleic acid present in a pharmaceutical composition of the invention may comprise a sequence of 6-50, in particular 10-30, 15-30 and 20-30, contiguous nucleotides of the nucleic acid coding for the tumor-associated antigen identified according to the invention.

[0034] In further embodiments, a tumor-associated antigen or a part thereof, provided by a pharmaceutical composition of the invention either directly or via expression of a nucleic acid, binds to MHC molecules on the surface of cells, said binding preferably causing a cytolytic response and/or inducing cytokine release.

[0035] A pharmaceutical composition of the invention may comprise a pharmaceutically compatible carrier and/or an adjuvant.

[0036] A pharmaceutical composition of the invention is preferably used for the treatment or prevention of a disease characterized by selective expression or abnormal expression of a tumor-associated nucleic acid and/or tumor-associated antigen. In a preferred embodiment, the disease is a neoplastic disease, preferably cancer.

[0037] In a preferred embodiment, the pharmaceutical composition of the invention is in the form of a vaccine which may be used therapeutically or prophylactically. Such vaccine preferably comprises a tumor-associated antigen identified according to the invention or a part thereof, and/or a nucleic acid which codes for a tumor-associated antigen identified according to the invention or a part thereof. In particular embodiments, the nucleic acid is present in a virus or host cell.

[0038] The invention furthermore relates to methods of treating, preventing, diagnosing or monitoring, i.e. determining the regression, progression, course and/or onset of, a disease characterized by expression or abnormal expression of one of more tumor-associated nucleic acids identified according to the invention, preferably also resulting in expression or abnormal expression of one of more tumor-associated antigens identified according to the invention, preferably a neoplastic disease, in particular cancer. In one embodiment, the treatment or prevention comprises administering a pharmaceutical composition of the invention.

[0039] The methods of diagnosing and/or methods of monitoring according to the invention generally concern the detection of and/or determination of the quantity of one or more parameters selected from the group consisting of (i) a tumor-associated nucleic acid identified according to the invention, or a part thereof, (ii) a tumor-associated antigen identified according to the invention, or a part thereof, (iii) an antibody against a tumor-associated antigen identified according to the invention or a part thereof, and (iv) T lymphocytes, preferably cytotoxic or T helper lymphocytes, which are specific for a tumor-associated antigen identified according to the invention or a part thereof and/or a complex between the tumor-associated antigen or a part thereof and an MHC molecule, in a biological sample isolated from a patient, preferably from a patient having said disease, being suspected of having or falling ill with said disease or having a potential for said disease. Means for accomplishing said detection and/or determination of the quantity are described herein and will be apparent to the skilled person.

[0040] Preferably, the presence of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes and/or a quantity of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes which is increased compared to a patient without said disease is indicative for the presence of said disease or a potential for a development of said disease.

[0041] The methods of diagnosing and/or monitoring of the invention also include embodiments wherein by detection or determination of the quantity of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes it is possible to assess and/or prognose the metastatic behavior of said disease, wherein, preferably, the presence of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes and/or a quantity of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes which is increased compared to a patient without said disease or without a metastasis of said disease is indicative for a metastatic behavior of said disease or a potential for a metastatic behavior of said disease.

[0042] In particular embodiments, said detection or determination of the quantity comprises (i) contacting a biological sample with an agent which binds specifically to said tumor-associated nucleic acid or said part thereof, to said tumor-associated antigen or said part thereof, to said antibody or to said T lymphocytes, and (ii) detecting the formation of or determining the amount of a complex between the agent and the nucleic acid or the part thereof, the tumor-associated antigen or the part thereof, the antibody, or the T lymphocytes.

[0043] In one embodiment, the disease is characterized by expression or abnormal expression of two or more different tumor-associated nucleic acids preferably also resulting in expression or abnormal expression of two or more different tumor-associated antigens and a detection or determination of the quantity comprises a detection or determination of the quantity of two or more different tumor-associated nucleic acids or of parts thereof, of two or more different tumor-associated antigens or of parts thereof, of two or more antibodies binding to said two or more different tumor-associated antigens or to parts thereof and/or of two or more T lymphocytes specific for said two or more different tumor-associated antigens or parts thereof, or complexes thereof with MHC molecules. In a further embodiment, the biological sample isolated from the patient is compared to a comparable normal biological sample.

[0044] The methods of monitoring according to the invention preferably comprise a detection of and/or determination of the quantity of one or more of the parameters mentioned above in a first sample at a first point in time and in a further sample at a second point in time, wherein the course of the disease is determined by comparing the two samples.

[0045] Preferably, a level of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes which is increased in a sample compared to a sample taken earlier from a patient indicates that the patient has developed or is about to develop cancer and/or a metastasis of cancer and/or a relapse of cancer. Preferably, a level of said nucleic acid or said part thereof, said tumor-associated antigen or said part thereof, said antibody and/or said T lymphocytes which is decreased in a sample compared to a sample taken earlier

from a patient indicates regression of cancer and/or a metastasis of cancer in said patient and thus, preferably indicates a successful cancer therapy.

[0046] According to the invention, detection of a nucleic acid or of a part thereof or determining the quantity of a nucleic acid or of a part thereof may be carried out using an oligo- or polynucleotide probe which hybridizes specifically to said nucleic acid or said part thereof or may be carried out by selective amplification of said nucleic acid or said part thereof, e.g. by means of PCR amplification. In one embodiment, the oligo- or polynucleotide probe comprises a sequence of 6-50, in particular 10-30, 15-30 and 20-30, contiguous nucleotides of said nucleic acid.

[0047] In particular embodiments, the tumor-associated antigen or the part thereof which is to be detected or the quantity of which is to be determined in the methods of the present invention is present intracellularly, on the cell surface or in a complex with an MHC molecule.

[0048] According to the invention, detection of a tumor-associated antigen or of a part thereof or determining the quantity of a tumor-associated antigen or of a part thereof may be carried out using an antibody binding specifically to said tumor-associated antigen or said part thereof.

[0049] According to the invention, detection of an antibody or determining the quantity of an antibody may be carried out using a protein or peptide binding specifically to said antibody.

[0050] According to the invention, detection of or determining the quantity of T lymphocytes which are specific for a tumor-associated antigen or a part thereof and/or a complex thereof with an MHC molecule may be carried out using a cell presenting the complex between said tumor-associated antigen or said part thereof and an MHC molecule. T lymphocytes may additionally be detected by detecting their proliferation, their cytokine production, and their cytotoxic activity triggered by specific stimulation with a complex of an MHC molecule and a tumor-associated antigen or a part thereof. T lymphocytes may also be detected with aid of a recombinant MHC molecule or a complex of two or more MHC molecules loaded with immunogenic fragments of one or more tumor-associated antigens.

[0051] An agent which is used for detection or determining the quantity in the methods of the invention such as an oligo- or polynucleotide probe, an antibody, a protein or peptide or a cell is preferably labeled in a detectable manner, in particular by a detectable marker such as a radioactive marker or an enzymic marker.

[0052] In a particular aspect, the invention relates to a method of treating, preventing, diagnosing or monitoring a disease characterized by expression or abnormal expression of a tumor-associated antigen identified according to the invention, which method comprises administering an antibody which binds to said tumor-associated antigen or to a part thereof and which is coupled to a therapeutic or diagnostic agent. The antibody may be a monoclonal antibody. In further embodiments, the antibody is a chimeric or humanized antibody or a fragment of an antibody.

[0053] In certain embodiments, the methods of the invention of diagnosing or monitoring a disease are performed with a biological sample containing or suspected of containing disseminating tumor cells or metastatic tumor cells. Such biological samples include, for example, blood, serum, bone marrow, sputum, bronchial aspirate, and/or bronchial lavage. Preferably, the methods of the invention of diagnosing or monitoring a disease are performed with a biological sample not containing placental cells and, in particular, being a non-placenta biological sample isolated from a subject.

[0054] In one particular aspect, the invention relates to a method of treating a patient having a disease characterized by expression or abnormal expression of a tumor-associated antigen identified according to the invention, which method comprises (i) providing a sample containing immunoreactive cells, either obtained from said patient or from another individual of the same species, in particular a healthy individual, or an individual of a different species, (ii) contacting said sample with a host cell expressing said tumor-associated antigen or a part thereof, under conditions which favor production of cytolytic T cells against said tumor-associated antigen or a part thereof, and (iii) introducing the cytolytic T cells into the patient in an amount suitable for lysing cells expressing the tumor-associated antigen or a part thereof. In one embodiment, the method includes cloning of the T cell receptor of cytolytic T cells obtained and transferring the nucleic acid coding for the T cell receptor to T cells, either obtained from said patient or from another individual of the same species, in particular a healthy individual, or an individual of a different species, which T cells thus receive the desired specificity and, as under (iii), may be introduced into the patient.

[0055] In one embodiment, the host cell endogenously expresses an MHC molecule. In a further embodiment, the host cell recombinantly expresses an MHC molecule and/or the tumor-associated antigen or the part thereof. Preferably, the host cell presents the tumor-associated antigen or the part thereof by MHC molecules on its surface. The host cell is preferably nonproliferative. In a preferred embodiment, the host cell is an antigen-presenting cell, in particular a dendritic cell, a monocyte or a macrophage.

[0056] The invention also relates to a method of treating a disease characterized by expression or abnormal expression of a tumor-associated antigen identified according to the invention, which method comprises (i) identifying cells from the patient which express abnormal amounts of the tumor-associated antigen, (ii) isolating a sample of said cells, (iii) culturing said cells, and (iv) introducing said cells into the patient in an amount suitable for triggering an immune response to the cells.

[0057] The present invention furthermore relates to a nucleic acid selected from the group consisting of (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-540, 541, 545, 549,

553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

5 **[0058]** In a further aspect, the invention relates to a recombinant nucleic acid molecule, in particular DNA or RNA molecule, which comprises a nucleic acid of the invention.

[0059] The invention also relates to host cells which contain a nucleic acid or recombinant nucleic acid molecule of the invention.

10 **[0060]** The host cell may also comprise a nucleic acid coding for a MHC molecule. In one embodiment, the host cell endogenously expresses the MHC molecule. In a further embodiment, the host cell recombinantly expresses the MHC molecule and/or the nucleic acid or recombinant nucleic acid molecule of the invention or a part thereof. Preferably, the host cell is nonproliferative. In a preferred embodiment, the host cell is an antigen-presenting cell, in particular a dendritic cell, a monocyte or a macrophage.

15 **[0061]** In a further embodiment, the invention relates to oligonucleotides which hybridize with a nucleic acid identified according to the invention and which may be used as genetic probes or as "antisense" molecules. Nucleic acid molecules in the form of oligonucleotide primers or competent probes, which hybridize with a nucleic acid identified according to the invention or parts thereof, may be used for detecting said nucleic acid and/or finding nucleic acids which are homologous to said nucleic acid identified according to the invention, e.g. by PCR amplification, Southern and Northern hybridization. Hybridization may be carried out under low stringency, more preferably under medium stringency and most preferably under high stringency conditions.

20 **[0062]** In a further aspect, the invention relates to a protein or peptide which is encoded by a nucleic acid selected from the group consisting of (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-540, 541, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof, (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions, (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c). In a preferred embodiment, the protein or peptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 542, 546, 550, 554, 567, 571, 584, 588, 592, 596, 603, 607, 614, 621, and 625 of the sequence listing, a part or derivative thereof.

25 **[0063]** In a further aspect, the invention relates to an immunogenic fragment of a tumor-associated antigen identified according to the invention. Said fragment preferably binds to a MHC molecule or an antibody, preferably to a human HLA receptor or a human antibody. According to the invention, a part or fragment preferably comprises a sequence of at least 5, at least 6, in particular at least 8, at least 10, at least 12, at least 15, at least 20, at least 30 or at least 50, amino acids.

30 **[0064]** In a further aspect, the invention relates to an agent which binds to a tumor-associated antigen identified according to the invention or to a part thereof. In a preferred embodiment, the agent is a protein or peptide, in particular an antibody, a T cell receptor or an MHC molecule. In further embodiments, the antibody is a monoclonal, chimeric, or humanized antibody, an antibody produced by combinatory techniques, or a fragment of an antibody. In one preferred embodiment, the invention relates to an antibody which binds selectively to a complex of (i) a tumor-associated antigen identified according to the invention or a part thereof and (ii) an MHC molecule to which said tumor-associated antigen identified according to the invention or said part thereof binds, with said antibody not binding to (i) or (ii) alone.

35 **[0065]** According to the invention, the term "binding" preferably relates to a specific binding. "Specific binding" means that an agent such as an antibody binds stronger to a target such as an epitope for which it is specific compared to the binding to another target. An agent binds stronger to a first target compared to a second target if it binds to the first target with a dissociation constant (K_D) which is lower than the dissociation constant for the second target. Preferably the dissociation constant (K_D) for the target to which the agent binds specifically is more than 10-fold, preferably more than 20-fold, more preferably more than 50-fold, even more preferably more than 100-fold, 200-fold, 500-fold or 1000-fold lower than the dissociation constant (K_D) for the target to which the agent does not bind specifically.

[0066] Such specific antibodies may, for example, be obtained by immunization using the aforementioned peptides.

40 **[0067]** The invention furthermore relates to a conjugate between an agent of the invention which binds to a tumor-associated antigen identified according to the invention or to a part thereof or an antibody of the invention and a therapeutic or diagnostic agent. In one embodiment, the therapeutic or diagnostic agent is a toxin.

45 **[0068]** In a further aspect, the invention relates to a kit for detecting a disease characterized by expression or abnormal expression of one of more tumor-associated nucleic acids identified according to the invention, preferably also resulting in expression or abnormal expression of one of more tumor-associated antigens identified according to the invention, preferably a neoplastic disease, in particular cancer, which kit comprises agents for detection or determining the quantity (i) of the tumor-associated nucleic acid or of a part thereof, (ii) of the tumor-associated antigen or of a part thereof, (iii) of antibodies which bind to the tumor-associated antigen or to a part thereof, and/or (iv) of T cells which are specific for the tumor-associated antigen or a part thereof or a complex thereof with an MHC molecule. Such agents are described

herein above.

[0069] Specifically, the invention provides the following:

1. A pharmaceutical composition, comprising an agent which

(I) inhibits expression or activity of a tumor-associated antigen and/or
 (II) has tumor-inhibiting activity, and is selective for cells expressing or abnormally expressing a tumor-associated antigen and/or
 (III) when administered, selectively increases the amount of complexes between an MHC molecule and a tumor-associated antigen or a part thereof,
 said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of:

(a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
 (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
 (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
 (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

2. The pharmaceutical composition as claimed in item 1, in which the agent under (II) causes induction of cell death, reduction in cell growth, damage to the cell membrane or secretion of cytokines.

3. The pharmaceutical composition as claimed in item 1, in which the agent under (I) or (II) is an antisense nucleic acid which hybridizes selectively with the nucleic acid coding for the tumor-associated antigen.

4. The pharmaceutical composition as claimed in item 1, in which the agent under (I) or (II) is an antibody which binds selectively to the tumor-associated antigen.

5. The pharmaceutical composition as claimed in item 1, in which the agent comprises one or more components selected from the group consisting of:

(i) the tumor-associated antigen or a part thereof,
 (ii) a nucleic acid which codes for the tumor-associated antigen or a part thereof,
 (iii) an antibody which binds to the tumor-associated antigen or a part thereof,
 (iv) an antisense nucleic acid which hybridizes specifically with a nucleic acid coding for the tumor-associated antigen,
 (v) an siRNA directed against a nucleic acid coding for the tumor-associated antigen,
 (vi) a host cell which expresses the tumor-associated antigen or a part thereof, and
 (vii) isolated complexes between the tumor-associated antigen or a part thereof and an MHC molecule.

6. The pharmaceutical composition as claimed in item 1, in which the agent comprises two or more agents which in each case selectively inhibit expression or activity of different tumor-associated antigens, which are in each case selective for cells expressing or abnormally expressing different tumor-associated antigens or which increase the amount of complexes between MHC molecules and different tumor-associated antigens or parts thereof, with at least one of said tumor-associated antigens having a sequence encoded by a nucleic acid which is selected from the group consisting of:

(a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
 (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
 (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
 (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

7. A pharmaceutical composition, comprising one or more components selected from the group consisting of:

(i) a tumor-associated antigen or a part thereof,

- (ii) a nucleic acid which codes for a tumor-associated antigen or a part thereof,
- (iii) an antibody which binds to a tumor-associated antigen or a part thereof,
- (iv) an antisense nucleic acid which hybridizes specifically with a nucleic acid coding for a tumor-associated antigen,
- (v) an siRNA directed against a nucleic acid coding for a tumor-associated antigen,
- (vi) a host cell which expresses a tumor-associated antigen or a part thereof, and
- (vii) isolated complexes between a tumor-associated antigen or a part thereof and an MHC molecule, said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

8. The pharmaceutical composition as claimed in item 5 or 7, in which the nucleic acid of (ii) is present in an expression vector.

9. The pharmaceutical composition as claimed in item 5 or 7, in which the host cell secretes the tumor-associated antigen or the part thereof.

10. The pharmaceutical composition as claimed in item 5 or 7, in which the host cell additionally expresses an MHC molecule which binds to the tumor-associated antigen or the part thereof.

11. The pharmaceutical composition as claimed in item 10, in which the host cell expresses the MHC molecule and/or the tumor-associated antigen or the part thereof in a recombinant manner.

12. The pharmaceutical composition as claimed in item 10, in which the host cell expresses the MHC molecule endogenously.

13. The pharmaceutical composition as claimed in item 5, 7, 10 or 12, in which the host cell is an antigen-presenting cell.

14. The pharmaceutical composition as claimed in item 4, 5 or 7, in which the antibody is a monoclonal, chimeric or humanized antibody, or is a fragment of an antibody.

15. The pharmaceutical composition as claimed in item 4, 5, 7, or 14 in which the antibody is coupled to a therapeutic or diagnostic agent.

16. The pharmaceutical composition as claimed in any of items 1-15, which may be used for the treatment or prevention of cancer.

17. The pharmaceutical composition as claimed in item 16, in which the cancer is a lung tumor, a breast tumor, a prostate tumor, a melanoma, a colon tumor, a gastric tumor, a pancreatic tumor, an ENT tumor, an ovarian tumor, a colorectal tumor, a cervical carcinoma, a colon carcinoma or a mammary carcinoma.

18. The pharmaceutical composition as claimed in any of items 1, 2, 5-13, 16 and 17, which is in the form of a vaccine.

19. The pharmaceutical composition as claimed in item 18 for therapeutic and/or prophylactic use.

20. A method of diagnosing or monitoring a cancer disease, which method comprises detecting or determining the quantity

- (i) of a tumor-associated nucleic acid or of a part thereof, and/or
- (ii) of a tumor-associated antigen or of a part thereof, and/or
- (iii) of an antibody to the tumor-associated antigen or a part thereof and/or

(iv) of T lymphocytes which are specific to the tumor-associated antigen or to a part thereof in a biological sample isolated from a patient, said tumor-associated nucleic acid being selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
 - (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
 - (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
 - (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c), and
- said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from said group of nucleic acids.

21. The method as claimed in item 20, in which the detection or determination of the quantity comprises

- (i) contacting the biological sample with an agent which binds specifically to the tumor-associated nucleic acid or to the part thereof, to the tumor-associated antigen or the part thereof, to the antibody or to the T lymphocytes, and
- (ii) detecting the formation of or determining the quantity of a complex between the agent and the nucleic acid or the part thereof, the tumor-associated antigen or the part thereof, the antibody or the T lymphocytes.

22. The method as claimed in item 21, in which the agent which binds specifically to the tumor-associated nucleic acid or to the part thereof is an oligonucleotide or polynucleotide, which hybridizes specifically to said nucleic acid or to said part thereof.

23. The method as claimed in item 21, in which the agent which binds specifically to the tumor-associated antigen or the part thereof is an antibody binding specifically to said tumor-associated antigen or to said part thereof.

24. The method as claimed in item 21, in which the agent which binds specifically to the antibody is a protein or peptide binding specifically to said antibody.

25. The method as claimed in item 21, in which the agent which binds specifically to the T lymphocytes is a cell presenting the complex between the tumor-associated antigen or the part thereof and an MHC molecule.

26. The method as claimed in any of items 20 to 25 wherein said monitoring of said disease comprises determining regression, course or onset of said disease in a sample from a patient who has said disease or is suspected of falling ill with said disease.

27. The method as claimed in item 26, which comprises a detection or determination of the quantity in a first sample at a first point in time and in a further sample at a second point in time and a comparison of the two samples.

28. The method as claimed in any of items 21-27, in which the agent is labeled in a detectable manner.

29. The method as claimed in any of items 20-28, in which the sample comprises body fluid and/or body tissue.

30. The method as claimed in any of items 20-29, in which said cancer disease is characterized by expression or abnormal expression of said tumor-associated nucleic acid.

31. The method as claimed in item 30, in which said cancer disease is further characterized by expression or abnormal expression of a tumor-associated antigen encoded by said tumor-associated nucleic acid.

32. A method of treating or preventing a disease characterized by expression or abnormal expression of a tumor-associated antigen, which method comprises administration of a pharmaceutical composition as claimed in any of items 1-19,

said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610,

- 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

33. A method of treating, preventing, diagnosing or monitoring a disease characterized by expression or abnormal expression of a tumor-associated antigen, which method comprises administering an antibody binding to said tumor-associated antigen or to a part thereof and coupled to a therapeutic or diagnostic agent, said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

34. The method as claimed in item 23 or 33, in which the antibody is a monoclonal, chimeric or humanized antibody, or is a fragment of an antibody.

35. A method of treating a patient having a disease characterized by expression or abnormal expression of a tumor-associated antigen, which method comprises:

- (i) providing a sample containing immunoreactive cells,
- (ii) contacting said sample with a host cell expressing said tumor-associated antigen or a part thereof, under conditions which favor production of cytolytic or cytokine-releasing T cells against said tumor-associated antigen or said part thereof, and
- (iii) introducing the cytolytic or cytokine-releasing T cells into the patient in an amount suitable for lysing cells expressing the tumor-associated antigen or a part thereof, said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

36. The method as claimed in item 35, in which the host cell recombinantly expresses an MHC molecule binding to the tumor-associated antigen or to a part thereof.

37. The method as claimed in item 35, in which the host cell endogenously expresses an MHC molecule binding to the tumor-associated antigen or to a part thereof.

38. A method of inhibiting the development of cancer in a patient, which method comprises administering an effective amount of a pharmaceutical composition as claimed in any of items 1-19.

39. An agent, which binds specifically to a protein or polypeptide or to a part thereof, said protein or polypeptide being encoded by a nucleic acid selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

40. The agent as claimed in item 39, which is an antibody.

41. The agent as claimed in item 40, in which the antibody is a monoclonal, chimeric or humanized antibody, or is a fragment of an antibody.

42. An antibody, which binds selectively to a complex of:

- (i) a protein or polypeptide or a part thereof and
- (ii) an MHC molecule to which said protein or polypeptide or said part thereof binds, with said antibody not binding to (i) or (ii) alone and said protein or polypeptide being encoded by a nucleic acid selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

43. The antibody as claimed in item 42, which is a monoclonal, chimeric or humanized antibody, or is a fragment of an antibody.

44. A conjugate between an agent as claimed in any of items 39-41 or an antibody as claimed in any of items 42-43 and a therapeutic or diagnostic agent.

45. The conjugate as claimed in item 44, in which the therapeutic or diagnostic agent is a toxin.

46. A kit for detecting cancer, which kit comprises agents for detecting or determining the quantity

- (i) of a tumor-associated nucleic acid or of a part thereof, and/or
 - (ii) of a tumor-associated antigen or of a part thereof, and/or
 - (iii) of antibodies which bind to the tumor-associated antigen or to a part thereof, and/or
 - (iv) of T cells which are specific for a complex between the tumor-associated antigen or a part thereof and an MHC molecule,
- said tumor-associated nucleic acid being selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 541, 1-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
 - (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
 - (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
 - (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c), and
- said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from said group of nucleic acids.

47. The pharmaceutical composition as claimed in any of items 1-19 or the method as claimed in any of items 20-38 in which the tumor-associated antigen comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 542, 546, 550, 554, 567, 571, 584, 588, 592, 596, 603, 607, 614, 621, and 625, a part or derivative thereof.

48. The agent as claimed in any of items 39-41, the antibody as claimed in any of items 42-43 or the conjugate as claimed in any of items 44-45 in which the protein or polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs: 542, 546, 550, 554, 567, 571, 584, 588, 592, 596, 603, 607, 614, 621, and 625, a part or derivative thereof.

Detailed description of the invention

[0070] A reference herein to a range of numerical values is to be understood so as to specify and mention each of the

individual numerical values comprised by said range. For example, a reference to SEQ ID NOs: 1-540 is to be understood so as to refer to each and every of the following individual SEQ ID NOs: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, and 540.

[0071] According to the invention, a "reference" such as a reference sample or reference organism may be used to correlate and compare the results obtained in the methods of the invention from a test sample or test organism, i.e. a patient. Typically the reference organism is a healthy organism, in particular an organism which does not suffer from cancer.

[0072] A "reference value" can be determined from a reference empirically by measuring a sufficiently large number of references. Preferably the reference value is determined by measuring at least 2, preferably at least 3, preferably at least 5, preferably at least 8, preferably at least 12, preferably at least 20, preferably at least 30, preferably at least 50, or preferably at least 100 references.

[0073] According to the invention, a nucleic acid is preferably deoxyribonucleic acid (DNA) or ribonucleic acid (RNA). Nucleic acids comprise according to the invention genomic DNA, cDNA, mRNA, recombinantly produced and chemically synthesized molecules. According to the invention, a nucleic acid may be present as a single-stranded or double-stranded and linear or covalently circularly closed molecule.

[0074] The terms "tumor-associated nucleic acid identified according to the invention" and "nucleic acid encoding a tumor-associated antigen identified according to the invention" have similar meanings. However, the different terms are used herein to account for the fact that in some embodiments only the expression of nucleic acid, in particular mRNA, is of relevance while the expression of protein is not a critical factor.

[0075] As used herein, the term "RNA" means a molecule comprising at least one ribonucleotide residue. By "ribonucleotide" is meant a nucleotide with a hydroxyl group at the 2'-position of a beta-D-ribo-furanose moiety. The term includes double stranded RNA, single stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as altered RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of a RNA or internally, for example at one or more nucleotides of the RNA. Nucleotides in RNA molecules can also comprise non-standard nucleotides, such as non-naturally occurring nucleotides or chemically synthesized nucleotides or deoxynucleotides. These altered RNAs can be referred to as analogs or analogs of naturally-occurring RNA.

[0076] If reference is made herein to the detection of or the determination of the quantity of a nucleic acid, the nucleic acid which is actually to be detected or the quantity of which is actually to be determined is preferably mRNA. However, it should be understood that this may also include embodiments wherein mRNA is detected or the quantity of mRNA is determined indirectly. For example, mRNA may be transformed into cDNA and the cDNA detected or its quantity determined. mRNA is given herein as the cDNA equivalent. One skilled in the art would understand that the cDNA sequence is equivalent to the mRNA sequence, and can be used for the same purpose herein, e.g., the generation of probes hybridizing to the nucleic acid to be detected. Thus, if reference is made herein to the sequences shown in the sequence listing this is also to include the RNA equivalents of said sequences.

[0077] The nucleic acids described according to the invention have preferably been isolated. The term "isolated nucleic

acid" means according to the invention that the nucleic acid was (i) amplified in vitro, for example by polymerase chain reaction (PCR), (ii) recombinantly produced by cloning, (iii) purified, for example by cleavage and gel-electrophoretic fractionation, or (iv) synthesized, for example by chemical synthesis. An isolated nucleic acid is a nucleic acid which is available for manipulation by recombinant DNA techniques.

[0078] A degenerate nucleic acid according to the invention is a nucleic acid that differs from a reference nucleic acid in codon sequence due to the degeneracy of the genetic code.

[0079] "Derivative" of a nucleic acid means according to the invention that single or multiple such as at least 2, at least 4, or at least 6 and preferably up to 3, up to 4, up to 5, up to 6, up to 10, up to 15, or up to 20 nucleotide substitutions, deletions and/or additions are present in said nucleic acid. Furthermore, the term "derivative" also comprises chemical derivatization of a nucleic acid on a nucleotide base, on the sugar or on the phosphate. The term "derivative" also comprises nucleic acids which contain nucleotides and nucleotide analogs not occurring naturally.

[0080] Preferably the degree of identity between a specific nucleic acid sequence described herein and a nucleic acid sequence which is a derivative of said specific nucleic acid sequence, which hybridizes with said specific nucleic acid sequence and/or which is degenerate with respect to said specific nucleic acid sequence will be at least 70%, preferably at least 75%, preferably at least 80%, more preferably at least 85%, even more preferably at least 90% or most preferably at least 95%, 96%, 97%, 98% or 99%. The degree of identity is preferably given for a region of at least about 30, at least about 50, at least about 70, at least about 90, at least about 100, at least about 150, at least about 200, at least about 250, at least about 300, or at least about 400 nucleotides. In preferred embodiments, the degree of identity is given for the entire length of the reference nucleic acid sequence, such as the nucleic acid sequences given in the sequence listing.

[0081] A nucleic acid is "complementary" to another nucleic acid if the two sequences are capable of hybridizing and forming a stable duplex with one another, with hybridization preferably being carried out under conditions which allow specific hybridization between polynucleotides (stringent conditions). Stringent conditions are described, for example, in Molecular Cloning: A Laboratory Manual, J. Sambrook et al., Editors, 2nd Edition, Cold Spring Harbor Laboratory press, Cold Spring Harbor, New York, 1989 or Current Protocols in Molecular Biology, F.M. Ausubel et al., Editors, John Wiley & Sons, Inc., New York and refer, for example, to hybridization at 65°C in hybridization buffer (3.5 x SSC, 0.02% Ficoll, 0.02% polyvinylpyrrolidone, 0.02% bovine serum albumin, 2.5 mM NaH₂PO₄ (pH 7), 0.5% SDS, 2 mM EDTA). SSC is 0.15 M sodium chloride/0.15 M sodium citrate, pH 7. After hybridization, the membrane to which the DNA has been transferred is washed, for example, in 2 x SSC at room temperature and then in 0.1-0.5 x SSC/0.1 x SDS at temperatures of up to 68°C.

[0082] A percent complementarity indicates the percentage of contiguous residues in a nucleic acid molecule that can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" or "fully complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a second nucleic acid sequence. Preferably, the degree of complementarity according to the invention is at least 70%, preferably at least 75%, preferably at least 80%, more preferably at least 85%, even more preferably at least 90% or most preferably at least 95%, 96%, 97%, 98% or 99%.

[0083] "Sequence similarity" indicates the percentage of amino acids that either are identical or that represent conservative amino acid substitutions. "Sequence identity" between two polypeptide or nucleic acid sequences indicates the percentage of amino acids or nucleotides that are identical between the sequences.

[0084] The term "percentage identity" is intended to denote a percentage of nucleotides or of amino acid residues which are identical between the two sequences to be compared, obtained after the best alignment, this percentage being purely statistical and the differences between the two sequences being distributed randomly and over their entire length. Sequence comparisons between two nucleotide or amino acid sequences are conventionally carried out by comparing these sequences after having aligned them optimally, said comparison being carried out by segment or by "window of comparison" in order to identify and compare local regions of sequence similarity. The optimal alignment of the sequences for comparison may be produced, besides manually, by means of the local homology algorithm of Smith and Waterman, 1981, *Adv. App. Math.* 2, 482, by means of the local homology algorithm of Needleman and Wunsch, 1970, *J. Mol. Biol.* 48, 443, by means of the similarity search method of Pearson and Lipman, 1988, *Proc. Natl Acad. Sci. USA* 85, 2444, or by means of computer programs which use these algorithms (GAP, BESTFIT, FASTA, BLAST P, BLAST N and TFASTA in Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.).

[0085] The percentage identity is calculated by determining the number of identical positions between the two sequences being compared, dividing this number by the number of positions compared and multiplying the result obtained by 100 so as to obtain the percentage identity between these two sequences.

[0086] In one embodiment, a nucleic acid sequence which is a derivative of a specific nucleic acid sequence, which is degenerate with respect to a specific nucleic acid sequence or which is a part of a specific nucleic acid sequence has a relevant function and/or activity of the specific nucleic acid sequence, i.e. it may encode a protein or peptide having the same activity or immunological properties as the protein or peptide encoded by the specific nucleic acid sequence and, in one embodiment, encodes the same protein or peptide.

[0087] Nucleic acids coding for tumor-associated antigens may, according to the invention, be present alone or in combination with other nucleic acids, in particular heterologous nucleic acids. In preferred embodiments, a nucleic acid is functionally linked to expression control sequences or regulatory sequences which may be homologous or heterologous with respect to said nucleic acid. A coding sequence and a regulatory sequence are "functionally" linked to one another, if they are covalently linked to one another in such a way that expression or transcription of said coding sequence is under the control or under the influence of said regulatory sequence. If the coding sequence is to be translated into a functional protein, then, with a regulatory sequence functionally linked to said coding sequence, induction of said regulatory sequence results in transcription of said coding sequence, without causing a frame shift in the coding sequence or said coding sequence not being capable of being translated into the desired protein or peptide.

[0088] The term "expression control sequence" or "regulatory sequence" comprises according to the invention promoters, enhancers and other control elements which regulate expression of a gene. In particular embodiments of the invention, the expression control sequences can be regulated. The exact structure of regulatory sequences may vary as a function of the species or cell type, but generally comprises 5'untranscribed and 5'untranslated sequences which are involved in initiation of transcription and translation, respectively, such as TATA box, capping sequence, CAAT sequence, and the like. More specifically, 5'untranscribed regulatory sequences comprise a promoter region which includes a promoter sequence for transcriptional control of the functionally linked gene. Regulatory sequences may also comprise enhancer sequences or upstream activator sequences.

[0089] According to the invention, a nucleic acid may furthermore be present in combination with another nucleic acid which codes for a peptide controlling secretion of the protein or peptide encoded by said nucleic acid from a host cell. According to the invention, a nucleic acid may also be present in combination with another nucleic acid which codes for a peptide causing the encoded protein or peptide to be anchored on the cell membrane of the host cell or compartmentalized into particular organelles of said cell. Similarly, a combination with a nucleic acid is possible which represents a reporter gene or any "tag".

[0090] In a preferred embodiment, a recombinant nucleic acid molecule is according to the invention a vector, where appropriate with a promoter, which controls expression of a nucleic acid, for example a nucleic acid coding for a tumor-associated antigen identified according to the invention. The term "vector" is used here in its most general meaning and comprises any intermediary vehicle for a nucleic acid which enables said nucleic acid, for example, to be introduced into prokaryotic and/or eukaryotic cells and, where appropriate, to be integrated into a genome. Vectors of this kind are preferably replicated and/or expressed in the cells. An intermediary vehicle may be adapted, for example, to the use in electroporation, in bombardment with microprojectiles, in liposomal administration, in the transfer with the aid of agrobacteria or in insertion via DNA or RNA viruses. Vectors comprise plasmids, phagemids, bacteriophages or viral genomes.

[0091] The nucleic acids coding for a tumor-associated antigen identified according to the invention may be used for transfection of host cells. Nucleic acids here mean both recombinant DNA and RNA. Recombinant RNA may be prepared by in-vitro transcription of a DNA template. Furthermore, it may be modified by stabilizing sequences, capping and polyadenylation prior to application.

[0092] According to the invention, the term "host cell" relates to any cell which can be transformed or transfected with an exogenous nucleic acid. The term "host cells" comprises according to the invention prokaryotic (e.g. *E. coli*) or eukaryotic cells (e.g. dendritic cells, B cells, CHO cells, COS cells, K562 cells, yeast cells and insect cells). Particular preference is given to mammalian cells such as cells from humans, mice, hamsters, pigs, goats, primates. The cells may be derived from a multiplicity of tissue types and comprise primary cells and cell lines. Specific examples comprise keratinocytes, peripheral blood leukocytes, stem cells of the bone marrow and embryonic stem cells. In further embodiments, the host cell is an antigen-presenting cell, in particular a dendritic cell, monocyte or a macrophage. A nucleic acid may be present in the host cell in the form of a single copy or of two or more copies and, in one embodiment, is expressed in the host cell.

[0093] According to the invention, the term "expression" is used in its most general meaning and comprises the production of RNA or of RNA and protein. It also comprises partial expression of nucleic acids. Furthermore, expression may be carried out transiently or stably. Preferred expression systems in mammalian cells comprise pcDNA3.1 and pRc/CMV (Invitrogen, Carlsbad, CA), which contain a selectable marker such as a gene imparting resistance to G418 (and thus enabling stably transfected cell lines to be selected) and the enhancer-promoter sequences of cytomegalovirus (CMV).

[0094] In those cases of the invention in which a MHC molecule presents a tumor-associated antigen or a part thereof, an expression vector may also comprise a nucleic acid sequence coding for said MHC molecule. The nucleic acid sequence coding for the MHC molecule may be present on the same expression vector as the nucleic acid coding for the tumor-associated antigen or the part thereof, or both nucleic acids may be present on different expression vectors. In the latter case, the two expression vectors may be cotransfected into a cell. If a host cell expresses neither the tumor-associated antigen or the part thereof nor the MHC molecule, both nucleic acids coding therefor may be transfected into the cell either on the same expression vector or on different expression vectors. If the cell already expresses the MHC molecule, only the nucleic acid sequence coding for the tumor-associated antigen or the part thereof can be transfected

into the cell.

[0095] The invention also comprises kits for detection and/or determination of the quantity of nucleic acids. Such kits comprise, for example, a pair of amplification primers which hybridize to the nucleic acid which is to be detected or the amount of which is to be determined. The primers preferably comprise a sequence of 6-50, in particular 10-30, 15-30 and 20-30 contiguous nucleotides of the nucleic acid and are nonoverlapping, in order to avoid the formation of primer dimers. One of the primers will hybridize to one strand of the nucleic acid, and the other primer will hybridize to the complementary strand in an arrangement which allows amplification of the nucleic acid.

[0096] "Antisense molecules" or "antisense nucleic acids" may be used for regulating, in particular reducing, expression of a nucleic acid. The term "antisense molecule" or "antisense nucleic acid" refers according to the invention to an oligonucleotide which is an oligoribonucleotide, oligodeoxyribonucleotide, modified oligoribonucleotide or modified oligodeoxyribonucleotide and which hybridizes under physiological conditions to DNA comprising a particular gene or to mRNA of said gene, thereby inhibiting transcription of said gene and/or translation of said mRNA. According to the invention, an "antisense molecule" also comprises a construct which contains a nucleic acid or a part thereof in reverse orientation with respect to its natural promoter. An antisense transcript of a nucleic acid or of a part thereof may form a duplex with naturally occurring mRNA and thus prevent accumulation of or translation of the mRNA. Another possibility is the use of ribozymes for inactivating a nucleic acid.

[0097] Antisense oligonucleotides preferred according to the invention have a sequence of 6-50, in particular 10-30, 15-30 and 20-30, contiguous nucleotides of the target nucleic acid and preferably are fully complementary to the target nucleic acid or to a part thereof.

[0098] In preferred embodiments, the antisense oligonucleotide hybridizes with an N-terminal or 5' upstream site such as a translation initiation site, transcription initiation site or promoter site. In further embodiments, the antisense oligonucleotide hybridizes with a 3' untranslated region or mRNA splicing site.

[0099] In one embodiment, an oligonucleotide of the invention consists of ribonucleotides, deoxyribonucleotides or a combination thereof, with the 5' end of one nucleotide and the 3' end of another nucleotide being linked to one another by a phosphodiester bond. These oligonucleotides may be synthesized in the conventional manner or produced recombinantly.

[0100] In preferred embodiments, an oligonucleotide of the invention is a "modified" oligonucleotide. Here, the oligonucleotide may be modified in very different ways, without impairing its ability to bind its target, in order to increase, for example, its stability or therapeutic efficacy. According to the invention, the term "modified oligonucleotide" means an oligonucleotide in which (i) at least two of its nucleotides are linked to one another by a synthetic internucleoside bond (i.e. an internucleoside bond which is not a phosphodiester bond) and/or (ii) a chemical group which is usually not found in nucleic acids is covalently linked to the oligonucleotide. Preferred synthetic internucleoside bonds are phosphorothioates, alkyl phosphonates, phosphorodithioates, phosphate esters, alkyl phosphonothioates, phosphoramidates, carbamates, carbonates, phosphate triesters, acetamidates, carboxymethyl esters and peptides.

[0101] The term "modified oligonucleotide" also comprises oligonucleotides having a covalently modified base and/or sugar. "Modified oligonucleotides" comprise, for example, oligonucleotides with sugar residues which are covalently bound to low molecular weight organic groups other than a hydroxyl group at the 3' position and a phosphate group at the 5' position. Modified oligonucleotides may comprise, for example, a 2'-O-alkylated ribose residue or another sugar instead of ribose, such as arabinose.

[0102] It is to be understood that all embodiments described above with respect to oligonucleotides may also apply to polynucleotides.

[0103] By "small interfering RNA" or "siRNA" as used herein is meant an isolated RNA molecule, preferably greater than 10 nucleotides in length, more preferably greater than 15 nucleotides in length, and most preferably 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 nucleotides in length that is used to identify a target gene or mRNA to be degraded.

A range of 19-25 nucleotides is the most preferred size for siRNAs.

[0104] siRNA according to the invention can comprise partially purified RNA, substantially pure RNA, synthetic RNA, or recombinantly produced RNA, as well as altered RNA that differs from naturally-occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations can include addition of non-nucleotide material, such as to the end(s) of the siRNA or to one or more internal nucleotides of the siRNA; modifications that make the siRNA resistant to nuclease digestion (e. g., the use of 2'-substituted ribonucleotides or modifications to the sugar-phosphate backbone); or the substitution of one or more nucleotides in the siRNA with deoxyribonucleotides. Furthermore, siRNA may be modified to increase the stability thereof as described above for modified oligonucleotides, in particular by introducing one or more phosphorothioate linkages.

[0105] One or both strands of the siRNA can also comprise a 3'-overhang. As used herein, a "3'-overhang" refers to at least one unpaired nucleotide extending from the 3'-end of an RNA strand. Thus in one embodiment, the siRNA comprises at least one 3'-overhang of from 1 to about 6 nucleotides (which includes ribonucleotides or deoxynucleotides) in length, preferably from 1 to about 5 nucleotides in length, more preferably from 1 to about 4 nucleotides in length, and particularly preferably from about 2 to about 4 nucleotides in length. In the embodiment in which both strands of the

siRNA molecule comprise a 3'-overhang, the length of the overhangs can be the same or different for each strand. In a most preferred embodiment, the 3'-overhang is present on both strands of the siRNA, and is 2 nucleotides in length. For example, each strand of the siRNA of the invention can comprise 3'-overhangs of dideoxythymidylic acid ("TT") or diuridylic acid ("uu").

[0106] In order to enhance the stability of the siRNA, the 3'-overhangs can be also stabilized against degradation. In one embodiment, the overhangs are stabilized by including purine nucleotides, such as adenosine or guanosine nucleotides. Alternatively, substitution of pyrimidine nucleotides by modified analogues, e.g., substitution of uridine nucleotides in the 3'-overhangs with 2'-deoxythymidine, is tolerated and does not affect the efficiency of RNAi degradation. In particular, the absence of a 2'-hydroxyl in the 2'-deoxythymidine significantly enhances the nuclease resistance of the 3'-overhang in tissue culture medium. The sense and antisense strands of the siRNA can comprise two complementary, single-stranded RNA molecules or can comprise a single molecule in which two complementary portions are base-paired and are covalently linked by a single-stranded "hairpin" area. That is, the sense region and antisense region can be covalently connected via a linker molecule. The linker molecule can be a polynucleotide or non-nucleotide linker. Without wishing to be bound by any theory, it is believed that the hairpin area of the latter type of siRNA molecule is cleaved intracellularly by the "Dicer" protein (or its equivalent) to form a siRNA of two individual base-paired RNA molecules.

[0107] As used herein, "target mRNA" refers to an RNA molecule that is a target for downregulation.

[0108] siRNA can be expressed from pol III expression vectors without a change in targeting site, as expression of RNAs from pol III promoters is only believed to be efficient when the first transcribed nucleotide is a purine.

[0109] siRNA according to the invention can be targeted to any stretch of approximately 19-25 contiguous nucleotides in any of the target mRNA sequences (the "target sequence"). Techniques for selecting target sequences for siRNA are given, for example, in Tuschl T. et al., "The siRNA User Guide", revised Oct. 11, 2002, the entire disclosure of which is herein incorporated by reference. "The siRNA User Guide" is available on the world wide web at a website maintained by Dr. Thomas Tuschl, Laboratory of RNA Molecular Biology, Rockefeller University, New York, USA, and can be found by accessing the website of the Rockefeller University and searching with the keyword "siRNA". Thus, the sense strand of the present siRNA comprises a nucleotide sequence substantially identical to any contiguous stretch of about 19 to about 25 nucleotides in the target mRNA.

[0110] Generally, a target sequence on the target mRNA can be selected from a given cDNA sequence corresponding to the target mRNA, preferably beginning 50 to 100 nt downstream (i.e., in the 3'-direction) from the start codon. The target sequence can, however, be located in the 5'- or 3'-untranslated regions, or in the region nearby the start codon.

[0111] siRNA can be obtained using a number of techniques known to those of skill in the art. For example, siRNA can be chemically synthesized or recombinantly produced using methods known in the art, such as the *Drosophila* in vitro system described in U.S. published application 2002/0086356 of Tuschl et al., the entire disclosure of which is herein incorporated by reference.

[0112] Preferably, siRNA is chemically synthesized using appropriately protected ribonucleoside phosphoramidites and a conventional DNA/RNA synthesizer. siRNA can be synthesized as two separate, complementary RNA molecules, or as a single RNA molecule with two complementary regions.

[0113] Alternatively, siRNA can also be expressed from recombinant circular or linear DNA plasmids using any suitable promoter. Such embodiments are included according to the present invention when reference is made herein to the administration of siRNA or the incorporation of siRNA into pharmaceutical compositions. Suitable promoters for expressing siRNA of the invention from a plasmid include, for example, the U6 or H1 RNA pol III promoter sequences and the cytomegalovirus promoter.

[0114] Selection of other suitable promoters is within the skill in the art. The recombinant plasmids of the invention can also comprise inducible or regulatable promoters for expression of the siRNA in a particular tissue or in a particular intracellular environment.

[0115] The siRNA expressed from recombinant plasmids can either be isolated from cultured cell expression systems by standard techniques, or can be expressed intracellularly. The use of recombinant plasmids to deliver siRNA to cells in vivo is discussed in more detail below. siRNA can be expressed from a recombinant plasmid either as two separate, complementary RNA molecules, or as a single RNA molecule with two complementary regions.

[0116] Selection of plasmids suitable for expressing siRNA, methods for inserting nucleic acid sequences for expressing the siRNA into the plasmid, and methods of delivering the recombinant plasmid to the cells of interest are within the skill in the art.

[0117] siRNA can also be expressed from recombinant viral vectors intracellularly in vivo. The recombinant viral vectors comprise sequences encoding the siRNA and any suitable promoter for expressing the siRNA sequences. The recombinant viral vectors can also comprise inducible or regulatable promoters for expression of the siRNA in a particular tissue or in a particular intracellular environment. siRNA can be expressed from a recombinant viral vector either as two separate, complementary RNA molecules, or as a single RNA molecule with two complementary regions.

[0118] The term "peptide" comprises oligo- and polypeptides and refers to substances comprising two or more, preferably 3 or more, preferably 4 or more, preferably 6 or more, preferably 8 or more, preferably 10 or more, preferably 13

or more, preferably 16 more, preferably 21 or more and up to preferably 8, 10, 20, 30, 40 or 50, in particular 100 amino acids joined covalently by peptide bonds. The term "protein" refers to large peptides, preferably to peptides with more than 100 amino acid residues, but in general the terms "peptides" and "proteins" are synonyms and are used interchangeably herein.

[0119] Preferably, the proteins and peptides described according to the invention have been isolated. The terms "isolated protein" or "isolated peptide" mean that the protein or peptide has been separated from its natural environment. An isolated protein or peptide may be in an essentially purified state. The term "essentially purified" means that the protein or peptide is essentially free of other substances with which it is associated in nature or *in vivo*.

[0120] Such proteins and peptides may be used, for example, in producing antibodies and in an immunological or diagnostic assay or as therapeutics. Proteins and peptides described according to the invention may be isolated from biological samples such as tissue or cell homogenates and may also be expressed recombinantly in a multiplicity of pro- or eukaryotic expression systems.

[0121] For the purposes of the present invention, "derivatives" of a protein or peptide or of an amino acid sequence comprise amino acid insertion variants, amino acid deletion variants and/or amino acid substitution variants.

[0122] Amino acid insertion variants comprise amino- and/or carboxy-terminal fusions and also insertions of single or two or more amino acids in a particular amino acid sequence. In the case of amino acid sequence variants having an insertion, one or more amino acid residues are inserted into a particular site in an amino acid sequence, although random insertion with appropriate screening of the resulting product is also possible.

[0123] Amino acid deletion variants are characterized by the removal of one or more amino acids from the sequence.

[0124] Amino acid substitution variants are characterized by at least one residue in the sequence being removed and another residue being inserted in its place. Preference is given to the modifications being in positions in the amino acid sequence which are not conserved between homologous proteins or peptides and/or to replacing amino acids with other ones having similar properties.

[0125] "Conservative substitutions" may be made, for instance, on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the amphipathic nature of the residues involved. For example: (a) nonpolar (hydrophobic) amino acids include alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine; (b) polar neutral amino acids include glycine, serine, threonine, cysteine, tyrosine, asparagine, and glutamine; (c) positively charged (basic) amino acids include arginine, lysine, and histidine; and (d) negatively charged (acidic) amino acids include aspartic acid and glutamic acid. Substitutions typically may be made within groups (a)-(d). In addition, glycine and proline may be substituted for one another based on their ability to disrupt α -helices. Some preferred substitutions may be made among the following groups: (i) S and T; (ii) P and G; and (iii) A, V, L and I. Given the known genetic code, and recombinant and synthetic DNA techniques, the skilled scientist readily can construct DNAs encoding the conservative amino acid variants.

[0126] Preferably the degree of similarity, preferably identity between a specific amino acid sequence described herein and an amino acid sequence which is a derivative of said specific amino acid sequence will be at least 70%, preferably at least 80%, preferably at least 85%, even more preferably at least 90% or most preferably at least 95%, 96%, 97%, 98% or 99%. The degree of similarity or identity is given preferably for a region of at least about 20, at least about 40, at least about 60, at least about 80, at least about 100, at least about 120, at least about 140, at least about 160, at least about 200 or 250 amino acids. In preferred embodiments, the degree of similarity or identity is given for the entire length of the reference amino acid sequence.

[0127] In one embodiment, a protein or peptide which is a derivative of a specific protein or peptide or which is a part of a specific protein or peptide has a relevant function and/or activity of the specific protein or peptide, i.e. it may have the same activity or immunological properties as the specific protein or peptide.

[0128] The amino acid variants described above may be readily prepared with the aid of known peptide synthesis techniques such as, for example, by solid phase synthesis (Merrifield, 1964) and similar methods or by recombinant DNA manipulation. The manipulation of DNA sequences for preparing proteins and peptides having substitutions, insertions or deletions, is described in detail in Sambrook et al. (1989), for example.

[0129] According to the invention, "derivatives" of proteins and peptides also comprise single or multiple substitutions, deletions and/or additions of any molecules associated with the protein or peptide, such as carbohydrates, lipids and/or proteins or peptides. The term "derivative" also extends to all functional chemical equivalents of said proteins and peptides.

[0130] According to the invention, a part or fragment of a tumor-associated antigen preferably has a functional property of the protein or peptide from which it has been derived. Such functional properties comprise the interaction with antibodies, the interaction with other peptides or proteins, the selective binding of nucleic acids and an enzymatic activity. A particular property is the ability to form a complex with MHC molecules and, where appropriate, generate an immune response, preferably by stimulating cytotoxic or T helper cells. A part or fragment of a tumor-associated antigen preferably comprises a sequence of at least 6, in particular at least 8, at least 10, at least 12, at least 15, at least 20, at least 30 or at least 50, consecutive amino acids of the tumor-associated antigen. A part or fragment of a tumor-associated antigen preferably comprises a sequence of up to 8, in particular up to 10, up to 12, up to 15, up to 20, up to 30 or up to 55,

consecutive amino acids of the tumor-associated antigen. A part or fragment of a tumor-associated antigen is preferably a part of the tumor-associated antigen which corresponds to the non-transmembrane portion, in particular the extracellular portion of the antigen, or is comprised thereof.

[0131] Preferred parts or fragments of a tumor-associated antigen are in particular suitable for the stimulation of cytotoxic T-lymphocytes *in vivo* but also for the production of expanded and stimulated T-lymphocytes for the therapeutic adoptive transfer *ex vivo*.

[0132] A part or a fragment of a nucleic acid coding for a tumor-associated antigen relates according to the invention to the part of the nucleic acid, which codes at least for the tumor-associated antigen and/or for a part or a fragment of said tumor-associated antigen, as defined above. A part or fragment of a nucleic acid coding for a tumor-associated antigen is preferably that part of the nucleic acid corresponding to the open reading frame.

[0133] According to the invention, particular embodiments ought to involve providing "dominant negative" proteins or peptides derived from tumor-associated antigens. A dominant negative protein or peptide is an inactive protein or peptide variant which, by way of interacting with the cellular machinery, displaces an active protein or peptide from its interaction with the cellular machinery or which competes with the active protein or peptide, thereby reducing the effect of said active protein.

[0134] Antisera which contain specific antibodies specifically binding to the target protein can be prepared by various standard processes; see, for example, "Monoclonal Antibodies: A Practical Approach" by Philip Shepherd, Christopher Dean ISBN 0-19-963722-9; "Antibodies: A Laboratory Manual" by Ed Harlow, David Lane, ISBN: 0879693142 and "Using Antibodies: A Laboratory Manual: Portable Protocol NO" by Edward Harlow, David Lane, Ed Harlow ISBN 0879695447. Thereby it is also possible to generate affine and specific antibodies which recognize complex membrane proteins in their native form (Azorsa et al., J. Immunol. Methods 229: 35-48, 1999; Anderson et al., J. Immunol. 143: 1899-1904, 1989; Gardsvoll, J. Immunol. Methods 234: 107-116, 2000). This is in particular relevant for the preparation of antibodies which are to be used therapeutically, but also for many diagnostic applications. In this respect, it is possible to immunize with the whole protein, with extracellular partial sequences as well as with cells which express the target molecule in physiologically folded form.

[0135] Monoclonal antibodies are traditionally prepared using the hybridoma technology. (for technical details see: "Monoclonal Antibodies: A Practical Approach" by Philip Shepherd, Christopher Dean ISBN 0-19-963722-9; "Antibodies: A Laboratory Manual" by Ed Harlow, David Lane ISBN: 0879693142; "Using Antibodies: A Laboratory Manual: Portable Protocol NO" by Edward Harlow, David Lane, Ed Harlow ISBN: 0879695447).

[0136] It is known that only a small part of an antibody molecule, the paratope, is involved in binding of the antibody to its epitope (cf. Clark, W.R. (1986), The Experimental Foundations of Modern Immunology, Wiley & Sons, Inc., New York; Roitt, I. (1991), Essential Immunology, 7th Edition, Blackwell Scientific Publications, Oxford). The pFc' and Fc regions are, for example, effectors of the complement cascade but are not involved in antigen binding. An antibody from which the pFc' region has been enzymatically removed or which has been produced without the pFc' region, referred to as F(ab')₂ fragment, carries both antigen binding sites of a complete antibody. Similarly, an antibody from which the Fc region has been enzymatically removed or which has been produced without said Fc region, referred to as Fab fragment, carries one antigen binding site of an intact antibody molecule. Furthermore, Fab fragments consist of a covalently bound light chain of an antibody and part of the heavy chain of said antibody, referred to as Fd. The Fd fragments are the main determinants of antibody specificity (a single Fd fragment can be associated with up to ten different light chains, without altering the specificity of the antibody) and Fd fragments, when isolated, retain the ability to bind to an epitope.

[0137] Located within the antigen-binding part of an antibody are complementary-determining regions (CDRs) which interact directly with the antigen epitope and framework regions (FRs) which maintain the tertiary structure of the paratope. Both the Fd fragment of the heavy chain and the light chain of IgG immunoglobulins contain four framework regions (FR1 to FR4) which are separated in each case by three complementary-determining regions (CDR1 to CDR3). The CDRs and, in particular, the CDR3 regions and, still more particularly, the CDR3 region of the heavy chain are responsible to a large extent for antibody specificity.

[0138] Non-CDR regions of a mammalian antibody are known to be able to be replaced by similar regions of antibodies with the same or a different specificity, with the specificity for the epitope of the original antibody being retained. This made possible the development of "humanized" antibodies in which nonhuman CDRs are covalently linked to human FR and/or Fc/pFc' regions to produce a functional antibody.

[0139] As another example, WO 92/04381 describes the production and use of humanized murine RSV antibodies in which at least part of the murine FR regions have been replaced with FR regions of a human origin. Antibodies of this kind, including fragments of intact antibodies with antigen-binding capability, are often referred to as "chimeric" antibodies.

[0140] According to the invention, the term "antibody" also includes F(ab')₂, Fab, Fv, and Fd fragments of antibodies, chimeric antibodies, in which the Fc and/or FR and/or CDR1 and/or CDR2 and/or light chain-CDR3 regions have been replaced with homologous human or nonhuman sequences, chimeric F(ab')₂-fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain-CDR3 regions have been replaced with homologous human or nonhuman se-

quences, chimeric Fab-fragment antibodies in which the FR and/or CDR1 and/or CDR2 and/or light chain-CDR3 regions have been replaced with homologous human or nonhuman sequences, and chimeric Fd-fragment antibodies in which the FR and/or CDR1 and/or CDR2 regions have been replaced with homologous human or nonhuman sequences. The term "antibody" also comprises "single-chain" antibodies.

[0141] The invention also comprises proteins and peptides which bind specifically to tumor-associated antigens. Binding substances of this kind may be provided, for example, by degenerate peptide libraries which may be prepared simply in solution in an immobilized form or as phage-display libraries. It is likewise possible to prepare combinatorial libraries of peptides with one or more amino acids. Libraries of peptoids and nonpeptidic synthetic residues may also be prepared.

[0142] Antibodies may also be coupled to specific diagnostic substances for displaying cells and tissues expressing tumor-associated antigens. They may also be coupled to therapeutically useful substances.

[0143] Diagnostic substances or agents include any label that functions to: (i) provide a detectable signal; (ii) interact with a second label to modify the detectable signal provided by the first or second label, e.g. FRET (Fluorescence Resonance Energy Transfer); (iii) affect mobility, e.g. electrophoretic mobility, by charge, hydrophobicity, shape, or other physical parameters, or (iv) provide a capture moiety, e.g., affinity, antibody/antigen, or ionic complexation. Suitable as label are structures, such as fluorescent labels, luminescent labels, chromophore labels, radioisotopic labels, isotopic labels, preferably stable isotopic labels, isobaric labels, enzyme labels, particle labels, in particular metal particle labels, magnetic particle labels, polymer particle labels, small organic molecules such as biotin, ligands of receptors or binding molecules such as cell adhesion proteins or lectins, label-sequences comprising nucleic acids and/or amino acid residues which can be detected by use of binding agents, etc. Diagnostic substances comprise, in a nonlimiting manner, barium sulfate, iocetamic acid, iopanoic acid, calcium ipodate, sodium diatrizoate, meglumine diatrizoate, metrizamide, sodium tyropanoate and radio diagnostic, including positron emitters such as fluorine-18 and carbon-11, gamma emitters such as iodine-123, technetium-99m, iodine-131 and indium-111, nuclides for nuclear magnetic resonance, such as fluorine and gadolinium.

[0144] According to the invention, the terms "therapeutically useful substance", "therapeutic substance" or "therapeutic agent" means any molecule which may exert a therapeutic effect. According to the invention, a therapeutically useful substance is preferably selectively guided to a cell which expresses one or more tumor-associated antigens and includes anticancer agents, radioactive iodine-labeled compounds, toxins, cytostatic or cytolytic drugs, etc. Anticancer agents comprise, for example, aminoglutethimide, azathioprine, bleomycin sulfate, busulfan, carmustine, chlorambucil, cisplatin, cyclophosphamide, cyclosporine, cytarabine, dacarbazine, dactinomycin, daunorubin, doxorubicin, taxol, etoposide, fluorouracil, interferon- α , lomustine, mercaptopurine, methotrexate, mitotane, procarbazine HCl, thioguanine, vinblastine sulfate and vincristine sulfate. Other anticancer agents are described, for example, in Goodman and Gilman, "The Pharmacological Basis of Therapeutics", 8th Edition, 1990, McGraw-Hill, Inc., in particular Chapter 52 (Antineoplastic Agents (Paul Calabresi and Bruce A. Chabner). Toxins may be proteins such as pokeweed antiviral protein, cholera toxin, pertussis toxin, ricin, gelonin, abrin, diphtheria exotoxin or Pseudomonas exotoxin. Toxin residues may also be high energy-emitting radionuclides such as cobalt-60.

[0145] The term "major histocompatibility complex" or "MHC" relates to a complex of genes present in all vertebrates. MHC proteins or molecules are involved in signaling between lymphocytes and antigen presenting cells in normal immune reactions by binding peptides and presenting them for recognition by T cell receptors (TCR). MHC molecules bind peptides within an intracellular processing compartment and present these peptides on the surface of antigen presenting cells for recognition by T cells. The human MHC region also termed HLA is located on chromosome 6 and includes the class I and class II region. In one preferred embodiment of all aspects of the invention an MHC molecule is an HLA molecule.

[0146] "Reduce" or "inhibit" as used herein means the ability to cause an overall decrease, preferably of 20% or greater, more preferably of 50% or greater, and most preferably of 75% or greater, in the level, e.g. in the level of protein or mRNA as compared to a reference sample (e.g., a sample not treated with siRNA). This reduction or inhibition of RNA or protein expression can occur through targeted mRNA cleavage or degradation. Assays for protein expression or nucleic acid expression are known in the art and include, for example, ELISA, western blot analysis for protein expression, and northern blotting or RNase protection assays for RNA.

[0147] The term "patient" means according to the invention a human being, a nonhuman primate or another animal, in particular a mammal such as a cow, horse, pig, sheep, goat, dog, cat or a rodent such as a mouse and rat. In a particularly preferred embodiment, the patient is a human being.

[0148] According to the invention the term "increased" or "increased amount" preferably refers to an increase by at least 10%, in particular at least 20%, at least 50% or at least 100%. The amount of a substance is also increased in a test sample such as a biological sample compared to a reference sample if it is detectable in the test sample but absent or not detectable in the reference sample.

[0149] According to the invention, the term "disease" refers to any pathological state in which tumor-associated nucleic acids and/or tumor-associated antigens are expressed or abnormally expressed. "Abnormal expression" means according to the invention that expression is altered, preferably increased, compared to the state in a healthy individual. An

increase in expression refers to an increase by at least 10%, in particular at least 20%, at least 50% or at least 100%. In one embodiment, expression is only found in tissue of a diseased individual, while expression in a healthy individual is repressed or is repressed in a healthy individual except for placenta. One example of such a disease is cancer, wherein the term "cancer" according to the invention comprises leukemias, seminomas, melanomas, teratomas, lymphomas, neuroblastomas, gliomas, rectal cancer, endometrial cancer, kidney cancer, adrenal cancer, thyroid cancer, blood cancer, skin cancer, cancer of the brain, cervical cancer, intestinal cancer, liver cancer, colon cancer, stomach cancer, intestine cancer, head and neck cancer, gastrointestinal cancer, lymph node cancer, esophagus cancer, colorectal cancer, pancreas cancer, ear, nose and throat (ENT) cancer, breast cancer, prostate cancer, cancer of the uterus, ovarian cancer and lung cancer and the metastases thereof. Examples thereof are lung carcinomas, mamma carcinomas, prostate carcinomas, colon carcinomas, renal cell carcinomas, cervical carcinomas, or metastases of the cancer types or tumors described above. The term cancer according to the invention also comprises cancer metastases.

[0150] By "tumor" is meant an abnormal group of cells or tissue that grows by a rapid, uncontrolled cellular proliferation and continues to grow after the stimuli that initiated the new growth cease. Tumors show partial or complete lack of structural organization and functional coordination with the normal tissue, and usually form a distinct mass of tissue, which may be either benign or malignant.

[0151] By "metastasis" is meant the spread of cancer cells from its original site to another part of the body. The formation of metastasis is a very complex process and depends on detachment of malignant cells from the primary tumor, invasion of the extracellular matrix, penetration of the endothelial basement membranes to enter the body cavity and vessels, and then, after being transported by the blood, infiltration of target organs. Finally, the growth of a new tumor at the target site depends on angiogenesis. Tumor metastasis often occurs even after the removal of the primary tumor because tumor cells or components may remain and develop metastatic potential. In one embodiment, the term "metastasis" according to the invention relates to "distant metastasis" which relates to a metastasis which is remote from the primary tumor and the regional lymph node system.

[0152] According to the invention, a biological sample may be a tissue sample, including bodily fluids, and/or a cellular sample and may be obtained in the conventional manner such as by tissue biopsy, including punch biopsy, and by taking blood, bronchial aspirate, sputum, urine, feces or other body fluids. According to the invention, the term "biological sample" also includes fractions of biological samples. Preferably, the term "biological sample" according to the invention does not include samples derived from placental tissue.

[0153] According to the invention, the term "immunoreactive cell" means a cell which can mature into an immune cell (such as B cell, T helper cell, or cytolytic T cell) with suitable stimulation. Immunoreactive cells comprise CD34⁺ hematopoietic stem cells, immature and mature T cells and immature and mature B cells. If production of cytolytic or T helper cells recognizing a tumor-associated antigen is desired, the immunoreactive cell is contacted with a cell expressing a tumor-associated antigen under conditions which favor production, differentiation and/or selection of cytolytic T cells and of T helper cells. The differentiation of T cell precursors into a cytolytic T cell, when exposed to an antigen, is similar to clonal selection of the immune system.

[0154] The terms "T cell" and "T lymphocyte" are used interchangeably herein and include T helper cells and cytotoxic T cells which comprise cytolytic T cells.

[0155] Some therapeutic methods are based on a reaction of the immune system of a patient, which results in a lysis of antigen-presenting cells such as cancer cells which present one or more tumor-associated antigens. In this connection, for example autologous cytotoxic T lymphocytes specific for a complex of a tumor-associated antigen and an MHC molecule are administered to a patient having a cellular abnormality. The production of such cytotoxic T lymphocytes in vitro is known. An example of a method of differentiating T cells can be found in WO-A-9633265. Generally, a sample containing cells such as blood cells is taken from the patient and the cells are contacted with a cell which presents the complex and which can cause propagation of cytotoxic T lymphocytes (e.g. dendritic cells). The target cell may be a transfected cell such as a COS cell. These transfected cells present the desired complex on their surface and, when contacted with cytotoxic T lymphocytes, stimulate propagation of the latter. The clonally expanded autologous cytotoxic T lymphocytes are then administered to the patient.

[0156] In another method of selecting antigen-specific cytotoxic T lymphocytes, fluorogenic tetramers of MHC class I molecule/peptide complexes are used for obtaining specific clones of cytotoxic T lymphocytes (Altman et al., Science 274:94-96, 1996; Dunbar et al., Curr. Biol. 8:413-416, 1998).

[0157] The present invention also includes therapeutic methods referred to as adoptive transfer (Greenberg, J. Immunol. 136(5):1917, 1986; Riddel et al., Science 257:238, 1992; Lynch et al., Eur. J. Immunol. 21:1403-1410, 1991; Kast et al., Cell 59:603-614, 1989), wherein cells presenting the desired complex (e.g. dendritic cells) are combined with cytotoxic T lymphocytes of the patient to be treated, resulting in a propagation of specific cytotoxic T lymphocytes. The propagated cytotoxic T lymphocytes are then administered to a patient having a cellular anomaly characterized by particular abnormal cells presenting the specific complex. The cytotoxic T lymphocytes then lyse the abnormal cells, thereby achieving a desired therapeutic effect.

[0158] Furthermore, cells presenting the desired complex (e.g. dendritic cells) may be combined with cytotoxic T

lymphocytes of healthy individuals or another species (e.g. mouse) which may result in propagation of specific cytotoxic T lymphocytes with high affinity. The high affinity T cell receptor of these propagated specific T lymphocytes may be cloned and optionally humanized to a different extent, and the T cell receptors thus obtained then transduced via gene transfer, for example using retroviral vectors, into T cells of patients. Adoptive transfer may then be carried out using these genetically altered T lymphocytes (Stanislowski et al., Nat Immunol. 2:962-70, 2001; Kessels et al., Nat Immunol. 2:957-61, 2001).

[0159] Adoptive transfer is not the only form of therapy which can be applied according to the invention. Cytotoxic T lymphocytes may also be generated *in vivo* in a manner known per se. One method uses nonproliferative cells expressing the complex. The cells used here will be those which usually express the complex, such as irradiated tumor cells or cells transfected with one or both genes necessary for presentation of the complex (i.e. the antigenic peptide and the presenting MHC molecule). Another preferred form is the introduction of the tumor-associated antigen in the form of recombinant RNA which may be introduced into cells by liposomal transfer or by electroporation, for example. The resulting cells present the complex of interest and are recognized by autologous cytotoxic T lymphocytes which then propagate.

[0160] A similar effect can be achieved by combining the tumor-associated antigen or a fragment thereof with an adjuvant in order to make incorporation into antigen-presenting cells *in vivo* possible. The tumor-associated antigen or a fragment thereof may be represented as protein, as DNA (e.g. within a vector) or as RNA. The tumor-associated antigen is processed to produce a peptide partner for the MHC molecule, while a fragment thereof may be presented without the need for further processing. The latter is the case in particular, if these can bind to MHC molecules. Preference is given to administration forms in which the complete antigen is processed *in vivo* by a dendritic cell, since this may also produce T helper cell responses which are needed for an effective immune response (Ossendorp et al., Immunol Lett. 74:75-9, 2000; Ossendorp et al., J. Exp. Med. 187:693-702, 1998). In general, it is possible to administer an effective amount of the tumor-associated antigen to a patient by intradermal injection, for example. However, injection may also be carried out intranodally into a lymph node (Maloy et al., Proc Natl Acad Sci USA 98:3299-303, 2001).

[0161] The pharmaceutical compositions and methods of treatment described according to the invention may also be used for immunization or vaccination to therapeutically treat or prevent a disease described herein. According to the invention, the terms "immunization" or "vaccination" preferably relate to an increase in or activation of an immune response to an antigen. It is possible to use animal models for testing an immunizing effect on cancer by using a tumor-associated antigen or a nucleic acid coding therefor. For example, human cancer cells may be introduced into a mouse to generate a tumor, and one or more nucleic acids coding for tumor-associated antigens may be administered. The effect on the cancer cells (for example reduction in tumor size) may be measured as a measure for the effectiveness of an immunization by the nucleic acid.

[0162] As part of the composition for an immunization or a vaccination, preferably one or more tumor-associated antigens or stimulating fragments thereof are administered together with one or more adjuvants for inducing an immune response or for increasing an immune response. An adjuvant is a substance which is incorporated into the antigen or administered together with the latter and which enhances the immune response. Adjuvants may enhance the immune response by providing an antigen reservoir (extracellularly or in macrophages), activating macrophages and/or stimulating particular lymphocytes. Adjuvants are known and comprise in a nonlimiting way monophosphoryl lipid A (MPL, SmithKline Beecham), saponins such as QS21 (SmithKline Beecham), DQS21 (SmithKline Beecham; WO 96/33739), QS7, QS17, QS18 and QS-L1 (So et al., Mol. Cells 7:178-186, 1997), incomplete Freund's adjuvant, complete Freund's adjuvant, vitamin E, montanide, alum, CpG oligonucleotides (cf. Kreig et al., Nature 374:546-9, 1995) and various water-in-oil emulsions prepared from biologically degradable oils such as squalene and/or tocopherol. Preferably, the peptides are administered in a mixture with DQS21/MPL. The ratio of DQS21 to MPL is typically about 1:10 to 10:1, preferably about 1:5 to 5:1 and in particular about 1:1. For administration to humans, a vaccine formulation typically contains DQS21 and MPL in a range from about 1 µg to about 100 µg.

[0163] Other substances which stimulate an immune response of the patient may also be administered. It is possible, for example, to use cytokines in a vaccination, owing to their regulatory properties on lymphocytes. Such cytokines comprise, for example, interleukin-12 (IL-12) which was shown to increase the protective actions of vaccines (cf. Science 268:1432-1434, 1995), GM-CSF and IL-18.

[0164] There are a number of compounds which enhance an immune response and which therefore may be used in a vaccination. Said compounds comprise costimulating molecules provided in the form of proteins or nucleic acids such as B7-1 and B7-2 (CD80 and CD86, respectively).

[0165] The invention also provides for administration of nucleic acids, proteins or peptides. Proteins and peptides may be administered in a manner known per se. In one embodiment, nucleic acids are administered by *ex vivo* methods, i.e. by removing cells from a patient, genetic modification of said cells in order to incorporate a tumor-associated antigen and reintroduction of the altered cells into the patient. This generally comprises introducing a functional copy of a gene into the cells of a patient *in vitro* and reintroducing the genetically altered cells into the patient. The functional copy of the gene is under the functional control of regulatory elements which allow the gene to be expressed in the genetically altered cells. Transfection and transduction methods are known to the skilled worker. The invention also provides for

administering nucleic acids *in vivo* by using vectors such as viruses and target-controlled liposomes. If according to the invention reference is made to the administration or incorporation into pharmaceutical compositions of nucleic acids this includes embodiments wherein the nucleic acid is present in such vectors.

[0166] In a preferred embodiment, a virus or viral vector for administering a nucleic acid coding for a tumor-associated antigen is selected from the group consisting of adenoviruses, adeno-associated viruses, pox viruses, including vaccinia virus and attenuated pox viruses, Semliki Forest virus, retroviruses, Sindbis virus and Ty virus-like particles. Particular preference is given to adenoviruses and retroviruses. The retroviruses are typically replication-deficient (i.e. they are incapable of generating infectious particles).

[0167] Methods of introducing nucleic acids into cells *in vitro* or *in vivo* comprise transfection of nucleic acid calcium phosphate precipitates, transfection of nucleic acids associated with DEAE, transfection or infection with the above viruses carrying the nucleic acids of interest, liposome-mediated transfection, and the like. In particular embodiments, preference is given to directing the nucleic acid to particular cells. In such embodiments, a carrier used for administering a nucleic acid to a cell (e.g. a retrovirus or a liposome) may have a bound target control molecule. For example, a molecule such as an antibody specific for a surface membrane protein on the target cell or a ligand for a receptor on the target cell may be incorporated into or attached to the nucleic acid carrier. Preferred antibodies comprise antibodies which bind selectively a tumor-associated antigen. If administration of a nucleic acid via liposomes is desired, proteins binding to a surface membrane protein associated with endocytosis may be incorporated into the liposome formulation in order to make target control and/or uptake possible. Such proteins comprise capsid proteins or fragments thereof which are specific for a particular cell type, antibodies to proteins which are internalized, proteins addressing an intracellular site, and the like.

[0168] The therapeutic compositions of the invention may be administered in pharmaceutically compatible preparations. Such preparations may usually contain pharmaceutically compatible concentrations of salts, buffer substances, preservatives, carriers, supplementing immunity-enhancing substances such as adjuvants, e.g. CpG oligonucleotides, cytokines, chemokines, saponin, GM-CSF and/or RNA and, where appropriate, other therapeutically active compounds.

[0169] The therapeutically active compounds of the invention may be administered via any conventional route, including by injection or infusion. The administration may be carried out, for example, orally, intravenously, intraperitoneally, intramuscularly, subcutaneously or transdermally. Preferably, antibodies are therapeutically administered by way of a lung aerosol. Antisense nucleic acids are preferably administered by slow intravenous administration.

[0170] The compositions of the invention are administered in effective amounts. An "effective amount" refers to the amount which achieves a desired reaction or a desired effect alone or together with further doses. In the case of treatment of a particular disease or of a particular condition characterized by expression of one or more tumor-associated antigens, the desired reaction preferably relates to inhibition of the course of the disease. This comprises slowing down the progress of the disease and, in particular, interrupting or reversing the progress of the disease. The desired reaction in a treatment of a disease or of a condition may also be delay of the onset or a prevention of the onset of said disease or said condition. According to the invention, a diagnosis or treatment of cancer may also include the diagnosis or treatment of cancer metastases which have already formed or will form. According to the invention, the term "treatment" comprises therapeutic and prophylactic treatment, i.e. prevention.

[0171] An effective amount of a composition of the invention will depend on the condition to be treated, the severeness of the disease, the individual parameters of the patient, including age, physiological condition, size and weight, the duration of treatment, the type of an accompanying therapy (if present), the specific route of administration and similar factors.

[0172] The pharmaceutical compositions of the invention are preferably sterile and contain an effective amount of the therapeutically active substance to generate the desired reaction or the desired effect.

[0173] The doses administered of the compositions of the invention may depend on various parameters such as the type of administration, the condition of the patient, the desired period of administration, etc. In the case that a reaction in a patient is insufficient with an initial dose, higher doses (or effectively higher doses achieved by a different, more localized route of administration) may be used.

[0174] Generally, doses of the tumor-associated antigen of from 1 ng to 1 mg, preferably from 10 ng to 100 µg, are formulated and administered for a treatment or for generating or increasing an immune response. If the administration of nucleic acids (DNA and RNA) coding for tumor-associated antigens is desired, doses of from 1 ng to 0.1 mg are formulated and administered.

[0175] The pharmaceutical compositions of the invention are generally administered in pharmaceutically compatible amounts and in pharmaceutically compatible compositions. The term "pharmaceutically compatible" refers to a nontoxic material which does not interact with the action of the active component of the pharmaceutical composition. Preparations of this kind may usually contain salts, buffer substances, preservatives, carriers and, where appropriate, other therapeutically active compounds. When used in medicine, the salts should be pharmaceutically compatible. However, salts which are not pharmaceutically compatible may be used for preparing pharmaceutically compatible salts and are included in the invention. Pharmacologically and pharmaceutically compatible salts of this kind comprise in a nonlimiting way

those prepared from the following acids: hydrochloric, hydrobromic, sulfuric, nitric, phosphoric, maleic, acetic, salicylic, citric, formic, malonic, succinic acids, and the like. Pharmaceutically compatible salts may also be prepared as alkali metal salts or alkaline earth metal salts, such as sodium salts, potassium salts or calcium salts.

[0176] A pharmaceutical composition of the invention may comprise a pharmaceutically compatible carrier. According to the invention, the term "pharmaceutically compatible carrier" refers to one or more compatible solid or liquid fillers, diluents or encapsulating substances, which are suitable for administration to humans. The term "carrier" refers to an organic or inorganic component, of a natural or synthetic nature, in which the active component is combined in order to facilitate application. The components of the pharmaceutical composition of the invention are usually such that no interaction occurs which substantially impairs the desired pharmaceutical efficacy.

[0177] The pharmaceutical compositions of the invention may contain suitable buffer substances such as acetic acid in a salt, citric acid in a salt, boric acid in a salt and phosphoric acid in a salt.

[0178] The pharmaceutical compositions may, where appropriate, also contain suitable preservatives such as benzalkonium chloride, chlorobutanol, paraben and thimerosal.

[0179] The pharmaceutical compositions are usually provided in a uniform dosage form and may be prepared in a manner known per se. Pharmaceutical compositions of the invention may be in the form of capsules, tablets, lozenges, solutions, suspensions, syrups, elixirs or in the form of an emulsion, for example.

[0180] Compositions suitable for parenteral administration usually comprise a sterile aqueous or nonaqueous preparation of the active compound, which is preferably isotonic to the blood of the recipient. Examples of compatible carriers and solvents are Ringer solution and isotonic sodium chloride solution. In addition, usually sterile, fixed oils are used as solution or suspension medium.

[0181] The present invention is described in detail by the figures and examples below, which are used only for illustration purposes and are not meant to be limiting. Owing to the description and the examples, further embodiments which are likewise included in the invention are accessible to the skilled worker.

Figures:

[0182]

Fig. 1. Expression of a tumor-associated nucleic acid identified according to the present invention in normal tissues and cancer tissue

Significant expression of the nucleic acid sequence according to SEQ ID NO:540 was found only in placenta tissue and mamma carcinomas.

Fig. 2. Quantitative expression of a tumor-associated nucleic acid identified according to the present invention in normal tissues and cancer tissue

Quantitative RT-PCR showed selective expression of the nucleic acid sequence according to SEQ ID NO:540 in placenta tissue and mamma carcinomas.

Fig. 3. Quantitative expression of SEQ ID NO:540 mRNA in MCF-7 breast cancer cells

Real-time RT-PCR 24h after transfection with siRNA oligos showed that both SEQ ID NO:540-specific siRNAs (siRNA#1 (SEQ ID NO:630, 631), siRNA#2 (SEQ ID NO:632, 633)) induce robust silencing of SEQ ID NO:540 expression.

Fig. 4. Silencing of SEQ ID NO:540 expression by transfection with siRNA oligos results in impaired proliferation of MCF-7 breast cancer cells

Proliferation was quantified 96h after transfection with siRNAs by measuring incorporation of BrdU in newly synthesized DNA strands. These results show that SEQ ID NO:540 is a positive factor for the proliferation of breast cancer cells.

Fig. 5. Quantitative expression of SEQ ID NO:541 in normal tissues and cancer tissue

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:541 in lung cancer.

Fig. 6. Quantitative expression of SEQ ID NO:545 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:545 in malignant melanomas.

Fig. 7. Quantitative expression of SEQ ID NO:549 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:549 in ovarian

cancer.

Fig. 8. Quantitative expression of SEQ ID NO:553 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:553 in colon cancer and ovarian cancer.

Fig. 9. Quantitative expression of SEQ ID NO:557 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:557 in breast cancer.

Fig. 10. Quantitative expression of SEQ ID NO:560 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:560 in colon cancer and ovarian cancer.

Fig. 11. Quantitative expression of SEQ ID NO:563 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:563 in breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma.

Fig. 12. Quantitative expression of SEQ ID NO:566 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:566 in gastric cancer, breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma.

Fig. 13. Quantitative expression of SEQ ID NO:570 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:570 in ovarian cancer, lung cancer and melanoma.

Fig. 14. Quantitative expression of SEQ ID NO:574 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:574 in lung cancer and melanoma.

Fig. 15. Quantitative expression of SEQ ID NO:577 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:577 in gastric cancer, breast cancer and lung cancer.

Fig. 16. Quantitative expression of SEQ ID NO:580 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:580 in ovarian cancer and lung cancer.

Fig. 17. Quantitative expression of SEQ ID NO:583 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:583 in colon cancer, ovarian cancer and lung cancer.

Fig. 18. Quantitative expression of SEQ ID NO:587 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:587 in lung cancer.

Fig. 19. Quantitative expression of SEQ ID NO:591 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:591 in breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma.

Fig. 20. Quantitative expression of SEQ ID NO:595 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:595 in gastric cancer, colon cancer, ovarian cancer, lung cancer and melanoma.

Fig. 21. Quantitative expression of SEQ ID NO:599 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:599 in gastric cancer, breast cancer, lung cancer and melanoma.

Fig. 22. Quantitative expression of SEQ ID NO:602 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:602 in ovarian cancer and lung cancer.

Fig. 23. Quantitative expression of SEQ ID NO:606 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:606 in gastric cancer, colon cancer and lung cancer.

Fig. 24. Quantitative expression of SEQ ID NO:610 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:610 in gastric cancer, breast cancer and lung cancer.

Fig. 25. Quantitative expression of SEQ ID NO:613 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:613 in breast cancer, lung cancer and melanoma.

Fig. 26. Quantitative expression of SEQ ID NO:617 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:617 in lung cancer and melanoma.

Fig. 27. Quantitative expression of SEQ ID NO:620 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:620 in ovarian cancer and melanoma.

Fig. 28. Quantitative expression of SEQ ID NO:624 in normal tissues and cancer tissues

Real-time RT-PCR showed overexpression of the nucleic acid sequence according to SEQ ID NO:624 in gastric cancer and lung cancer.

Examples:

[0183] The techniques and methods mentioned herein are carried out in a manner known per se and are described, for example, in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd Edition (1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. All methods including the use of kits and reagents are carried out according to the manufacturers' information unless specifically indicated.

Example 1: Screening for placenta-specific genes aberrantly activated in tumors

Tissues and cell lines

[0184] Tissues were obtained as human surplus materials during routine diagnostic or therapeutic procedures and were stored at -80°C until use. Cell lines were purchased from the *American Type Culture Collection (ATCC)* and the *German Resource Collection of Microorganisms and Cell Culture (DSMZ)*.

RNA isolation and microarray hybridization

[0185] Total RNA was isolated using the RNeasy Mini Kit protocol (Qiagen). Quantification of isolated RNA was performed using UV-spectroscopy and the quality was determined both by A_{260}/A_{280} ratio and Agilent bioanalyzer (Agilent Technologies). Five micrograms total RNA were used for cDNA synthesis with 5 pmol μL^{-1} T7-oligo(dT)₂₄ primer and was performed at 43°C for 90 minutes with the "Superscript First-Strand Synthesis-System" for RT-PCR (Invitrogen). Second-strand synthesis was performed with complete cDNA. The cDNA solution was incubated at 16°C for 2 hours followed by an incubation step for 20 min with 6 U T4-DNA polymerase at 16°C and the reaction was stopped using 10 μL of 0.5 M EDTA. After purification of the double stranded cDNA using the GeneChip Sample Cleanup Module (Affymetrix) labeled cRNA was generated from the cDNA sample by an *in vitro* transcription reaction that was supplemented with biotin-11-CTP and biotin-16-UTP (Enzo Diagnostics) according to the manufacturer's instructions. The cRNA was quantified by A_{260} , and the quality was determined using the labchip bioanalyzer (Agilent). Only cRNA specimens with a high quality were selected for further analyses. Fragmented cRNA (15 μg) was used to prepare 300 μL hybridization cocktail (100 mM MES, 1 M NaCl, 20 mM EDTA, 0.01% Tween-20) containing 0.1 mg mL^{-1} of herring sperm DNA, and 0.5 mg mL^{-1} acetylated bovine serum albumine. Control cRNA was used in order to compare hybridization efficiencies between arrays and to standardize the quantification of measured transcript levels and was included as component of the 'Eu-

karyotic Hybridization Control kit' (Affymetrix, Santa Clara, CA, USA). The cocktails were heated to 95°C for 5 minutes, equilibrated at 45°C for 5 minutes, and clarified by centrifugation. The cocktail was hybridized to HG U133 Plus 2.0 arrays (Affymetrix) at 45°C for 16 hours. The arrays were washed and stained with a streptavidin-conjugated fluor using the GeneChip fluidics station protocol EukGE-WS2 (Affymetrix) according to the manufacturer's instructions. Arrays were scanned with an argon-ion laser confocal scanner (Hewlett-Packard, Santa Clara, CA) with detection at 570 nm. Data were extracted using Microarray Suite version 5.0 (Affymetrix) and linearly scaled to achieve an average intensity of 2,500 per gene. Text files were exported to determine the intensity of each interrogating oligonucleotide perfect match probe cells or mismatch probe cells. In addition, the ratios of 5'- and 3'-ends of mRNA were analyzed of six randomly selected specimens (two of each group) using microarray test-chips (Test3 Array) containing 24 human housekeeping/maintenance genes (Affymetrix) and RNA degradation was not observed.

Bioinformatic analysis

[0186] The GeneChip® Operating Software 1.4 (Affymetrix) and ArrayAssist software package 5.2 (Stratagene) were used for statistical analyses.

Results

[0187] Screening of samples from the 18 normal tissues shown below in table 1 and 30 tumor cell lines of different entities shown below in table 2 resulted in the sequences described herein which are expressed in placenta among the normal tissues investigated and in tumor cell lines.

Tab. 1 Tissues used for microarray expression analysis

Tissue	Number
Placenta	2
Testis	2
Mammary gland	2
Thymus	2
Skin	2
Liver	2
Colon	2
Esophagus	2
Stomach	2
Lung	2
Kidney	2
Lymph node	2
Skeletal muscle	2
Myocard	1
Brain	1
Cerebellum	1
resting PBMCs	2
activ. PBMCs	2

Tab. 2 Cell lines used for microarray expression analysis

Cell line	Tissue
BT-549	Breast cancer

(continued)

Cell line	Tissue
MDA-MB-231 metastasizing	Breast cancer
MDA-MB-231 non-metastatsizing	Breast cancer
MDA-MB-435S	Breast cancer
MDA-MB-468	Breast cancer
SK-BR-3	Breast cancer
Caov-3	Ovarian cancer
FU-OV	Ovarian cancer
NIH-OVCAR-3	Ovarian cancer
COLO-205	Colorectal cancer
HCT-116	Colorectal cancer
HCT-116 DKO	Colorectal cancer
HCT-15	Colorectal cancer
HT-29	Colorectal cancer
LOVO	Colorectal cancer
SW-480	Colorectal cancer
CPC-N	Lung cancer
LOU-NH-91	Lung cancer
SHP-77	Lung cancer
SK-MES-1	Lung cancer
NCI-H-187	Lung cancer
NCI-H-209	Lung cancer
NCI-H-522	Lung cancer
DU-145	Prostate cancer
LnCaP	Prostate cancer
PC-3	Prostate cancer
MEL-JUSO	Melanoma
Murowsky	Melanoma
SK-MEL-37	Melanoma
HELA	Cervical cancer

Example 2: Validation of the identified tumor-associated markers

1. Examination of RNA expression

[0188] The identified tumor-associated markers are first validated with the aid of RNA which is obtained from various tissues or from tissue-specific cell lines. Since the differential expression pattern of healthy tissue in comparison with tumor tissue is of decisive importance for the subsequent therapeutic application, the target genes are preferably characterized with the aid of these tissue samples.

[0189] Total RNA is isolated from native tissue samples or from tumor cell lines by standard methods of molecular biology. Said isolation may be carried out, for example, with the aid of the RNeasy Maxi kit (Qiagen, Cat. No. 75162) according to the manufacturer's instructions. This isolation method is based on the use of chaotropic reagent guanidinium isothiocyanate. Alternatively, acidic phenol can be used for isolation (Chomczynski & Sacchi, Anal. Biochem. 162:

156-159, 1987). After the tissue has been worked up by means of guanidinium isothiocyanate, RNA is extracted with acidic phenol, subsequently precipitated with isopropanol and taken up in DEPC-treated water.

[0190] 2-4 µg of the RNA isolated in this way are subsequently transcribed into cDNA, for example by means of Superscript II (Invitrogen) according to the manufacturer's protocol. cDNA synthesis is primed with the aid of random hexamers (e.g. Roche Diagnostics) according to standard protocols of the relevant manufacturer. For quality control, the cDNAs are amplified over 30 cycles, using primers specific for the p53 gene which is expressed only lowly. Only p53-positive cDNA samples will be used for the subsequent reaction steps.

[0191] The targets are analyzed in detail by carrying out an expression analysis by means of PCR or quantitative PCR (qPCR) on the basis of a cDNA archive which has been isolated from various normal and tumor tissues and from tumor cell lines. For this purpose, 0.5 µl of cDNA of the above reaction mixture is amplified by a DNA polymerase (e.g. 1 U of HotStarTaq DNA polymerase, Qiagen) according to the protocols of the particular manufacturer (total volume of the reaction mixture: 25-50 µl). Aside from said polymerase, the amplification mixture comprises 0.3 mM dNTPs, reaction buffer (final concentration 1 ×, depending on the manufacturer of the DNA polymerase) and in each case 0.3 mM gene-specific "sense" and "antisense" primers.

[0192] The specific primers of the target gene are, as far as possible, selected in such a way that they are located in two different exons so that genomic contaminations do not lead to false-positive results. In a non-quantitative end point PCR, the cDNA is typically incubated at 95°C for 15 minutes in order to denature the DNA and to activate the Hot-Start enzyme. Subsequently the DNA is amplified over 35 cycles (1 min at 95°C, 1 min at the primer-specific hybridization temperature (approx. 55-65°C), 1 min at 72°C to elongate the amplicons). Subsequently, 10 µl of the PCR mixture are applied to agarose gels and fractionated in the electric field. The DNA is made visible in the gels by staining with ethidium bromide and the PCR result is documented by way of a photograph.

[0193] As an alternative to conventional PCR, expression of a target gene may also be analyzed by quantitative real time PCR. Meanwhile various analytical systems are available for this analysis, of which the best known ones are the ABI PRISM sequence detection system (TaqMan, Applied Biosystems), the iCycler (Biorad) and the Light cycler (Roche Diagnostics). As described above, a specific PCR mixture is subjected to a run in the real time instruments. By adding a DNA-intercalating dye (e.g. ethidium bromide, CybrGreen), the newly synthesized DNA is made visible by specific light excitation (according to the dye manufacturers' information). A multiplicity of points measured during amplification enables the entire process to be monitored and the nucleic acid concentration of the target gene to be determined quantitatively. The PCR mixture is normalized by measuring a housekeeping gene (e.g. 18S RNA, β-actin). Alternative strategies via fluorescently labeled DNA probes likewise allow quantitative determination of the target gene of a specific tissue sample (see TaqMan applications from Applied Biosystems).

[0194] As shown in Fig. 1, placenta was confirmed in RT-PCR analyses as the only healthy tissue expressing the nucleic acid sequence according to SEQ ID NO:540. No significant expression was found in any other normal tissue. However, high and significant levels of expression were found in breast cancer.

[0195] Quantitative real-time RT-PCR analyses revealed that the nucleic acid sequence according to SEQ ID NO:540 was expressed in significant levels in the majority of breast cancer samples analyzed; cf. Fig. 2.

2. Cloning

[0196] The complete target gene which is required for further characterization of the tumor-associated marker is cloned according to common molecular-biological methods (e.g. in "Current Protocols in Molecular Biology", John Wiley & Sons Ltd., Wiley InterScience). In order to clone the target gene or to analyze its sequence, said gene is first amplified by a DNA polymerase having a proof reading function (e.g. pfu, Roche Diagnostics). The amplicon is then ligated by standard methods into a cloning vector. Positive clones are identified by sequence analysis and subsequently characterized with the aid of prediction programs and known algorithms.

3. Prediction of the protein

[0197] Genes found according to the invention (in particular those from the RefSeq XM domain) may require cloning of the full-length gene, determination of the open reading frame and deduction and analysis of the protein sequence.

[0198] In order to clone the full-length sequence, common protocols for the rapid amplification of cDNA ends and the screening of cDNA expression libraries with gene-specific probes may be used (Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd edition (1989), Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.).

[0199] After assembling the fragments found in this way, potential open reading frames (ORF) can be predicted using common prediction programs. Since the position of the PolyA tail and of polyadenylation motifs predetermines the orientation of the potential gene product, only the 3 reading frames of that particular orientation remain out of a possible 6 reading frames. The former often yield only one sufficiently large open reading frame which may code for a protein, while the other reading frames have too many stop codons and would not code for any realistic protein. In the case of

alternative open reading frames, identification of the authentic ORF is assisted by taking into account the Kozak criteria for optimal transcription initiation and by analyzing the deduced protein sequences which may arise. Said ORF is further verified by generating immune sera against proteins deduced from the potential ORFs and analyzing said immune sera for recognition of a real protein in tissues and cell lines.

4. Production of antibodies

[0200] The tumor-associated antigens identified according to the invention are characterized, for example, by using antibodies. The invention further comprises the diagnostic or therapeutic use of antibodies. Antibodies may recognize proteins in the native and/or denatured state (Anderson et al., J. Immunol. 143: 1899-1904, 1989; Gardsvoll, J. Immunol. Methods 234: 107-116, 2000; Kayyem et al., Eur. J. Biochem. 208: 1-8, 1992; Spiller et al., J. Immunol. Methods 224: 51-60, 1999).

[0201] Antisera comprising specific antibodies which specifically bind to the target protein may be prepared by various standard methods; cf., for example, "Monoclonal Antibodies: A Practical Approach" by Phillip Shepherd, Christopher Dean ISBN 0-19-963722-9, "Antibodies: A Laboratory Manual" by Ed Harlow, David Lane ISBN: 0879693142 and "Using Antibodies: A Laboratory Manual: Portable Protocol NO" by Edward Harlow, David Lane, Ed Harlow ISBN: 0879695447. It is also possible here to generate affine and specific antibodies which recognize complex membrane proteins in their native form (Azorsa et al., J. Immunol. Methods 229: 35-48, 1999; Anderson et al., J. Immunol. 143: 1899-1904, 1989; Gardsvoll, J. Immunol. Methods. 234: 107-116, 2000). This is especially important in the preparation of antibodies which are intended to be used therapeutically but also for many diagnostic applications. For this purpose, both the complete protein and extracellular partial sequences may be used for immunization.

[0202] Immunization and production of polyclonal antibodies Various immunization protocols are published. A species (e.g. rabbits, mice) is immunized by a first injection of the desired target protein. The immune response of the animal to the immunogen can be enhanced by a second or third immunization within a defined period of time (approx. 2-4 weeks after the previous immunization). Blood is taken from said animals and immune sera obtained, again after various defined time intervals (1st bleeding after 4 weeks, then every 2-3 weeks, up to 5 takings). The immune sera taken in this way comprise polyclonal antibodies which may be used to detect and characterize the target protein in Western blotting, by flow cytometry, immunofluorescence or immunohistochemistry.

[0203] The animals are usually immunized by any of four well-established methods, with other methods also in existence. The immunization may be carried out using peptides specific for the target protein, using the complete protein, or using extracellular partial sequences of a protein which can be identified experimentally or via prediction programs. Since the prediction programs do not always work perfectly, it is also possible to employ two domains separated from one another by a transmembrane domain. In this case, one of the two domains has to be extracellular, which may then be proved experimentally (see below). Immunization is offered commercially by different service providers.

(1) In the first case, peptides (length: 8-12 amino acids) are synthesized by in vitro methods (possibly carried out by a commercial service), and said peptides are used for immunization. Normally 3 immunizations are carried out (e.g. with a concentration of 5-100 µg/immunization).

(2) Alternatively, immunization may be carried out using recombinant proteins. For this purpose, the cloned DNA of the target gene is cloned into an expression vector and the target protein is synthesized, for example, cell-free *in vitro*, in bacteria (e.g. *E. coli*), in yeast (e.g. *S. pombe*), in insect cells or in mammalian cells, according to the conditions of the particular manufacturer (e.g. Roche Diagnostics, Invitrogen, Clontech, Qiagen). It is also possible to synthesize the target protein with the aid of viral expression systems (e.g. baculovirus, vacciniavirus, adenovirus). After it has been synthesized in one of said systems, the target protein is purified, normally by employing chromatographic methods. In this context, it is also possible to use for immunization proteins which have a molecular anchor as an aid for purification (e.g. His tag, Qiagen; FLAG tag, Roche Diagnostics; GST fusion proteins). A multiplicity of protocols can be found, for example, in "Current Protocols in Molecular Biology", John Wiley & Sons Ltd., Wiley InterScience. After the target protein has been purified, an immunization is carried out as described above.

(3) If a cell line is available which synthesizes the desired protein endogenously, it is also possible to use this cell line directly for preparing the specific antiserum. In this case, immunization is carried out by 1-3 injections with in each case approx. $1-5 \times 10^7$ cells.

(4) The immunization may also be carried out by injecting DNA (DNA immunization). For this purpose, the target gene is first cloned into an expression vector so that the target sequence is under the control of a strong eukaryotic promoter (e.g. CMV promoter). Subsequently, DNA (e.g. 1-10 µg per injection) is transferred as immunogen using a gene gun into capillary regions with a strong blood flow in an organism (e.g. mouse, rabbit). The transferred DNA

is taken up by the animal's cells, the target gene is expressed, and the animal finally develops an immune response to the target protein (Jung et al., *Mol. Cells* 12: 41-49, 2001; Kasinrer et al., *Hybrid Hybridomics* 21: 287-293, 2002).

Production of monoclonal antibodies

[0204] Monoclonal antibodies are traditionally produced with the aid of the hybridoma technology (technical details: see "Monoclonal Antibodies: A Practical Approach" by Philip Shepherd, Christopher Dean ISBN 0-19-963722-9; "Antibodies: A Laboratory Manual" by Ed Harlow, David Lane ISBN: 0879693142, "Using Antibodies: A Laboratory Manual: Portable Protocol NO" by Edward Harlow, David Lane, Ed Harlow ISBN: 0879695447). A new method which is also used is the "SLAM" technology. Here, B cells are isolated from whole blood and the cells are made monoclonal. Subsequently the supernatant of the isolated B cell is analyzed for its antibody specificity. In contrast to the hybridoma technology, the variable region of the antibody gene is then amplified by single-cell PCR and cloned into a suitable vector. In this manner production of monoclonal antibodies is accelerated (de Wildt et al., *J. Immunol. Methods* 207: 61-67, 1997).

5. Validation of the targets by protein-chemical methods using antibodies

[0205] The antibodies which can be produced as described above can be used to further analyse the target protein as follows:

Specificity of the antibody

[0206] Assays based on cell culture with subsequent Western blotting are most suitable for demonstrating the fact that an antibody binds specifically only to the desired target protein (various variations are described, for example, in "Current Protocols in Proteinchemistry", John Wiley & Sons Ltd., Wiley InterScience). For the demonstration, cells are transfected with a cDNA for the target protein, which is under the control of a strong eukaryotic promoter (e.g. cytomegalovirus promoter; CMV). A wide variety of methods (e.g. electroporation, liposome-based transfection, calcium phosphate precipitation) are well established for transfecting cell lines with DNA (e.g. Lemoine et al., *Methods Mol. Biol.* 75: 441-7, 1997). As an alternative, it is also possible to use cell lines which express the target gene endogenously (detection via target gene-specific RT-PCR). As a control, in the ideal case, homologous genes are cotransfected in the experiment, in order to be able to demonstrate in the following Western blot the specificity of the analyzed antibody.

[0207] In the subsequent Western blotting, cells from cell culture or tissue samples which might contain the target protein are lysed in a 1% strength SDS solution, and the proteins are denatured in the process. The lysates are fractionated according to size by electrophoresis on 8-15% strength denaturing polyacrylamide gels (contain 1% SDS) (SDS polyacrylamide gel electrophoresis, SDS-PAGE). The proteins are then transferred by one of a plurality of blotting methods (e.g. semi-dry electroblot; Biorad) to a specific membrane (e.g. nitrocellulose, Schleicher & Schüll). The desired protein can be visualized on this membrane. For this purpose, the membrane is first incubated with the antibody which recognizes the target protein (dilution approx. 1:20-1:200, depending on the specificity of said antibody), for 60 minutes. After a washing step, the membrane is incubated with a second antibody which is coupled to a marker (e.g. enzymes such as peroxidase or alkaline phosphatase) and which recognizes the first antibody. It is then possible to make the target protein visible on the membrane in a color or chemiluminescent reaction (e.g. ECL, Amersham Bioscience). An antibody with a high specificity for the target protein should in the ideal case only recognise the desired protein itself.

[0208] Localization of the target protein Various methods are used to confirm the membrane localization, identified in the in silico approach, of the target protein. An important and well-established method using the antibodies described above is immunofluorescence (IF). For this purpose, cells of established cell lines which either synthesize the target protein (detection of the RNA by RT-PCR or of the protein by Western blotting) or else have been transfected with plasmid DNA are utilized. A wide variety of methods (e.g. electroporation, liposome-based transfection, calcium phosphate precipitation) are well established for transfection of cell lines with DNA (e.g. Lemoine et al., *Methods Mol. Biol.* 75: 441-7, 1997). The plasmid transfected into the cells, in immunofluorescence, may encode the unmodified protein or else couple different amino acid markers to the target protein. The principle markers are, for example, the fluorescent green fluorescent protein (GFP) in various differentially fluorescent forms, short peptide sequences of 6-12 amino acids for which high-affinity and specific antibodies are available, or the short amino acid sequence Cys-Cys-X-X-Cys-Cys which can bind via its cysteines specific fluorescent substances (Invitrogen). Cells which synthesize the target protein are fixed, for example, with paraformaldehyde or methanol. The cells may then, if required, be permeabilized by incubation with detergents (e.g. 0.2% Triton X-100). The cells are then incubated with a primary antibody which is directed against the target protein or against one of the coupled markers. After a washing step, the mixture is incubated with a second antibody coupled to a fluorescent marker (e.g. fluorescein, Texas Red, Dako), which binds to the first antibody. The cells labeled in this way are then overlaid with glycerol and analyzed with the aid of a fluorescence microscope according to

the manufacturer's information. Specific fluorescence emissions are achieved in this case by specific excitation depending on the substances employed. The analysis usually permits reliable localization of the target protein, the antibody quality and the target protein being confirmed in double stainings with, in addition to the target protein, also the coupled amino acid markers or other marker proteins whose localization has already been described in the literature being stained. GFP and its derivatives represent a special case, being excitable directly and themselves fluorescing. The membrane permeability which may be controlled through the use of detergents, in immunofluorescence, allows demonstration of whether an immunogenic epitope is located inside or outside the cell. The prediction of the selected proteins can thus be supported experimentally. An alternative possibility is to detect extracellular domains by means of flow cytometry. For this purpose, cells are fixed under non-permeabilizing conditions (e.g. with PBS/Na azide/2% FCS/5 mM EDTA) and analyzed in a flow cytometer in accordance with the manufacturer's instructions. Only extracellular epitopes can be recognized by the antibody to be analyzed in this method. A difference from immunofluorescence is that it is possible to distinguish between dead and living cells by using, for example, propidium iodide or trypan blue, and thus avoid false-positive results.

[0209] Another important detection is by immunohistochemistry (IHC) on specific tissue samples. The aim of this method is to identify the localization of a protein in a functionally intact tissue aggregate. IHC serves specifically for (1) being able to estimate the amount of target protein in tumor and normal tissues, (2) analyzing how many cells in tumor and healthy tissues synthesize the target gene, and (3) defining the cell type in a tissue (tumor, healthy cells) in which the target protein is detectable. Alternatively, the amounts of protein of a target gene may be quantified by tissue immunofluorescence using a digital camera and suitable software (e.g. Tillvision, Till-photonics, Germany). The technology has frequently been published, and details of staining and microscopy can therefore be found, for example, in "Diagnostic Immunohistochemistry" by David J., MD Dabbs ISBN: 0443065667 or in "Microscopy, Immunohistochemistry, and Antigen Retrieval Methods: For Light and Electron Microscopy" ISBN: 0306467704. It should be noted that, owing to the properties of antibodies, different protocols have to be used (an example is described below) in order to obtain a meaningful result.

[0210] Normally, histologically defined tumor tissues and, as reference, comparable healthy tissues are employed in IHC. It is also possible to use as positive and negative controls cell lines in which the presence of the target gene is known through RT-PCR analyses. A background control must always be included. Formalin-fixed (another fixation method, for example with methanol, is also possible) and paraffin-embedded tissue pieces with a thickness of 4 μ m are applied to a glass support and deparaffinated with xylene, for example. The samples are washed with TBS-T and blocked in serum. This is followed by incubation with the first antibody (dilution: 1:2 to 1:2000) for 1-18 hours, with affinity-purified antibodies normally being used. A washing step is followed by incubation with a second antibody which is coupled to an alkaline phosphatase (alternative: for example peroxidase) and directed against the first antibody, for approx. 30-60 minutes. This is followed by a color reaction using alkaline phosphatase (cf., for example, Shi et al., J. Histochem. Cytochem. 39: 741-748, 1991; Shin et al., Lab. Invest. 64: 693-702, 1991). To demonstrate antibody specificity, the reaction can be blocked by previous addition of the immunogen.

Analysis of protein modifications

[0211] Secondary protein modifications such as, for example, N- or O-glycosylations or myristilations may impair or even completely prevent the accessibility of immunogenic epitopes and thus call into question the efficacy of antibody therapies. Moreover, it has frequently been demonstrated that the type and amount of secondary modifications differ in normal and tumor tissues (e.g. Durand & Seta, 2000; Clin. Chem. 46: 795-805; Hakomori, 1996; Cancer Res. 56: 5309-18). The analysis of these modifications is therefore essential to the therapeutic success of an antibody. Potential binding sites can be predicted by specific algorithms.

[0212] Analysis of protein modifications usually takes place by Western blotting (see above). Glycosylations which usually have a size of several kDa, especially lead to a larger total mass of the target protein, which can be fractionated in SDS-PAGE. To detect specific O- and N-glycosidic bonds, protein lysates are incubated prior to denaturation by SDS with O- or N-glycosylases (in accordance with their respective manufacturer's instructions, e.g. PNGase, endoglycosidase F, endoglycosidase H, Roche Diagnostics). This is followed by Western blotting as described above. Thus, if there is a reduction in the size of a target protein after incubation with a glycosidase, it is possible to detect a specific glycosylation and, in this way, also analyze the tumor specificity of a modification.

Functional analysis of the target gene

[0213] The function of the target molecule may be crucial for its therapeutic usefulness, so that functional analyses are an important component in the characterization of therapeutically utilizable molecules. The functional analysis may take place either in cells in cell culture experiments or else in vivo with the aid of animal models. This involves either switching off the gene of the target molecule by mutation (knockout) or inserting the target sequence into the cell or the

organism (knockin). Thus it is possible to analyze functional modifications in a cellular context firstly by way of the loss of function of the gene to be analyzed (loss of function). In the second case, modifications caused by addition of the analyzed gene can be analyzed (gain of function).

5 a. Functional analysis in cells

[0214] Transfection. In order to analyze the gain of function, the gene of the target molecule must be transferred into the cell. For this purpose, cells which allow synthesis of the target molecule are transfected with a DNA. Normally, the gene of the target molecule here is under the control of a strong eukaryotic promoter (e.g. cytomegalovirus promoter; CMV). A wide variety of methods (e.g. electroporation, liposome-based transfection, calcium phosphate precipitation) are well established for transfecting cell lines with DNA (e.g. Lemoine et al., *Methods Mol. Biol.* 75: 441-7, 1997). The gene may be synthesized either transiently, without genomic integration, or else stably, with genomic integration after selection with neomycin, for example.

[0215] RNA interference (siRNA). An inhibition of expression of the target gene, which may induce a complete loss of function of the target molecule in cells, may be generated by the RNA interference (siRNA) technology in cells (Hannon, GJ. 2002. RNA interference. *Nature* 418: 244-51; Czauderna et al. 2003. *Nucl. Acid Res.* 31: 670-82). For this purpose, cells are transfected with short, double-stranded RNA molecules of approx. 20-25 nucleotides in length, which are specific for the target molecule. An enzymic process then results in degradation of the specific RNA of the target gene and thus in reduced expression of the target protein and consequently enables the target gene to be functionally analyzed.

[0216] Cell lines which have been modified by means of transfection or siRNA may subsequently be analyzed in different ways. The most common examples are listed below.

1. Proliferation and cell cycle behavior

[0217] A multiplicity of methods for analyzing cell proliferation are established and are commercially supplied by various companies (e.g. Roche Diagnostics, Invitrogen; details of the assay methods are described in the numerous application protocols). The number of cells in cell culture experiments can be determined by simple counting or by colorimetric assays which measure the metabolic activity of the cells (e.g. wst-1, Roche Diagnostics). Metabolic assay methods measure the number of cells in an experiment indirectly via enzymic markers. Cell proliferation may be measured directly by analyzing the rate of DNA synthesis, for example by adding bromodeoxyuridine (BrdU), with the integrated BrdU being detected colorimetrically via specific antibodies.

2. Apoptosis and cytotoxicity

[0218] A large number of assay systems for detecting cellular apoptosis and cytotoxicity are available. A decisive characteristic is the specific, enzyme-dependent fragmentation of genomic DNA, which is irreversible and in any case results in death of the cell. Methods for detecting these specific DNA fragments are commercially obtainable. An additional method available is the TUNEL assay which can detect DNA single-strand breaks also in tissue sections. Cytotoxicity is mainly detected via an altered cell permeability which serves as marker of the vitality state of cells. This involves on the one hand the analysis of markers which can typically be found intracellularly in the cell culture supernatant. On the other hand, it is also possible to analyze the absorbability of dye markers which are not absorbed by intact cells. The best-known examples of dye markers are Trypan blue and propidium iodide, a common intracellular marker is lactate dehydrogenase which can be detected enzymatically in the supernatant. Different assay systems of various commercial suppliers (e.g. Roche Diagnostics, Invitrogen) are available.

3. Migration assay

[0219] The ability of cells to migrate is analyzed in a specific migration assay, preferably with the aid of a Boyden chamber (Corning Costar) (Cinamon G., Alon R. J. *Immunol. Methods.* 2003 Feb; 273(1-2):53-62; Stockton et al. 2001. *Mol. Biol. Cell.* 12: 1937-56). For this purpose, cells are cultured on a filter with a specific pore size. Cells which can migrate are capable of migrating through this filter into another culture vessel below. Subsequent microscopic analysis then permits determination of a possibly altered migration behavior induced by the gain of function or loss of function of the target molecule.

b. Functional analysis in animal models

[0220] A possible alternative of cell culture experiments for the analysis of target gene function are complicated in vivo experiments in animal models. Compared to the cell-based methods, these models have the advantage of being

able to detect faulty developments or diseases which are detectable only in the context of the whole organism. A multiplicity of models for human disorders are available by now (Abate-Shen & Shen. 2002. Trends in Genetics S1-5; Matsusue et al. 2003. J. Clin. Invest. 111:737-47). Various animal models such as, for example, yeast, nematodes or zebra fish have since been characterized intensively. However, models which are preferred over other species are mammalian animal models such as, for example, mice (*Mus musculus*) because they offer the best possibility of reproducing the biological processes in a human context. For mice, on the one hand transgenic methods which integrate new genes into the mouse genome have been established in recent years (gain of function; Jegstrup I. et al. 2003. Lab Anim. 2003 Jan.; 37(1):1-9). On the other hand, other methodical approaches switch off genes in the mouse genome and thus induce a loss of function of a desired gene (knockout models, loss of function; Zambrowicz BP & Sands AT. 2003. Nat. Rev. Drug Discov. 2003 Jan; 2(1):38-51; Niwa H. 2001. Cell Struct. Funct. 2001 Jun; 26(3):137-48); technical details have been published in large numbers.

[0221] After the mouse models have been generated, alterations induced by the transgene or by the loss of function of a gene can be analyzed in the context of the whole organism (Balling R, 2001. Ann. Rev. Genomics Hum. Genet. 2: 463-92). Thus it is possible to carry out, for example, behavior tests as well as to biochemically study established blood parameters. Histological analyses, immunohistochemistry or electron microscopy enable alterations to be characterized at the cellular level. The specific expression pattern of a gene can be detected by in-situ hybridization (Peters T. et al. 2003. Hum. Mol. Genet 12:2109-20).

Example 3: Detailed analysis of the identified tumor-associated markers

RNA-Isolation, RT-PCR and real-Time RT-PCR

[0222] RNA extraction, first-strand cDNA synthesis, RT-PCR and real-time RT-PCR was performed as previously described (Koslowski, M. et al., Cancer Res. 62, 6750-6755 (2002), Koslowski, M. et al., Cancer Res. 64, 5988-5993 (2004)). Real-time quantitative expression analysis was performed in a 40 cycle RT-PCR. After normalization to HPRT (sense 5'-TGA CAC TGG CAA AAC AAT GCA-3'; antisense 5'-GGT CCT TTT CAC CAG CAA GCT-3', 62°C annealing) gene-specific transcripts in tumor samples were quantified relative to normal tissues using $\Delta\Delta CT$ calculation.

siRNA Duplexes

[0223] The SEQ ID NO:540 siRNA duplexes (Qiagen, Hilden, Germany) were directed against target sequences 5'-NNC CAC AGA AGG UAC CAG UUA-3' (siRNA#1; sense (5'-CCA CAG AAG GUA CCA GUU AW-3'), antisense (5'-UAA CUG GUA CCU UCU GUG GUU-3')) and 5'-NNC AGC AAG ACU CCC UCU AAA-3' (siRNA#2; sense (5'-CAG CAA GAC UCC CUC UAA AUU-3'), antisense (5'-UCU AGA GGG AGU CUU GCU GW-3')) of the SEQ ID NO:540 mRNA sequence.

Cell proliferation analysis

[0224] 24 h after transfection with siRNA duplexes 1×10^4 cells were cultured for 48 h in medium supplemented with 10% FCS. Proliferation was analyzed by measuring the incorporation of BrdU into newly synthesized DNA strands using the DELFIA cell proliferation Kit (Perkin Elmer, Boston, MA) according to the manufacturer's instructions on a Wallac Victor² multi-label counter (Perkin Elmer, Boston, MA).

[0225] Fig. 3 shows the quantification of SEQ ID NO:540 mRNA expression in MCF-7 breast cancer cells by real-time RT-PCR 24h after transfection with siRNA oligos. Compared to non-transfected cells and cells transfected with non-silencing (ns) siRNA both SEQ ID NO:540-specific siRNAs (siRNA#1 (SEQ ID NO:630, 631), siRNA#2 (SEQ ID NO: 632, 633)) induce robust silencing of SEQ ID NO:540 expression.

[0226] Fig. 4 shows that silencing of SEQ ID NO:540 expression by transfection with siRNA oligos results in impaired proliferation of MCF-7 breast cancer cells. Proliferation was quantified 96h after transfection with siRNAs by measuring incorporation of BrdU in newly synthesized DNA strands. These results show that SEQ ID NO:540 is a positive factor for the proliferation of breast cancer cells.

[0227] The nucleotide sequence according to SEQ ID NO:541 was deduced from SEQ ID NO:65 and codes for a 177 aa protein (SEQ ID NO:542) of unknown function. Expression of SEQ ID NO:541 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:543, 544); see Fig. 5. In normal tissues SEQ ID NO:541 is highly expressed in placenta and shows only weak expression in thymus. SEQ ID NO:541 is over-expressed in lung cancer. Based on these expression results, SEQ ID NO:541 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for this particular tumor type.

[0228] The nucleotide sequence according to SEQ ID NO:545 was deduced from SEQ ID NO:249 and codes for a member of the solute carrier (SLC) group of membrane proteins (SEQ ID NO:546). As is typical of integral membrane

proteins, SLCs contain a number of hydrophobic transmembrane alpha helices connected to each other by hydrophilic intra- or extra-cellular loops. Depending on the SLC, these transporters are functional as either monomers or obligate homo- or hetero-oligomers. The protein encoded by SEQ ID NO:545 is a cell surface protein. Expression of SEQ ID NO:545 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:547, 548); see Fig. 6. Compared to normal tissues, SEQ ID NO:545 is overexpressed in malignant melanomas. Based on these expression results, SEQ ID NO:545 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for this particular tumor type.

[0229] The nucleotide sequence according to SEQ ID NO:549 was deduced from SEQ ID NO:4 and codes for a 763 aa protein (SEQ ID NO:550) of unknown function. The protein harbors two potential transmembrane domains and a typical fibronectin type III domain. Fibronectin is a high-molecular-weight extracellular matrix glycoprotein that binds to membrane spanning receptor proteins (integrins). In addition to integrins, they also bind extracellular matrix components such as collagen, fibrin and heparan sulfate. The protein encoded by SEQ ID NO:549 might represent a hitherto unknown new fibronectin-like protein. Expression of SEQ ID NO:549 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:551, 552); see Fig. 7. Compared to normal tissues, SEQ ID NO:549 is overexpressed in ovarian cancer. Based on these expression results, SEQ ID NO:549 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular of this particular tumor type.

[0230] The nucleotide sequence according to SEQ ID NO:553 was deduced from SEQ ID NO:156 and codes for a 496 aa protein (SEQ ID NO:554) of unknown function. The protein harbors a potential transmembrane protein. Expression of SEQ ID NO:553 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:555, 556); see Fig. 8. In normal tissues SEQ ID NO:553 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:553 is overexpressed in colon cancer and ovarian cancer. Based on these expression results, SEQ ID NO:553 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0231] The nucleotide sequence according to SEQ ID NO:557 was deduced from SEQ ID NO:273. SEQ ID NO:557 represents a partial cDNA with no apparent open reading frame. Expression of SEQ ID NO:557 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:558, 559); see Fig. 9. In normal tissues high expression of SEQ ID NO:557 is detectable in breast. Compared to normal tissues, SEQ ID NO:557 is overexpressed in breast cancer. Based on these expression results, SEQ ID NO:557 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for this particular tumor type.

[0232] The nucleotide sequence according to SEQ ID NO:560 was deduced from SEQ ID NO:135. SEQ ID NO:560 has no apparent open reading frame. Expression of SEQ ID NO:560 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:561, 562); see Fig. 10. In normal tissues expression of SEQ ID NO:560 is detectable in duodenum and colon. Compared to normal tissues, SEQ ID NO:560 is overexpressed in colon cancer and ovarian cancer. Based on these expression results, SEQ ID NO:560 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0233] The nucleotide sequence according to SEQ ID NO:563 was deduced from SEQ ID NO:177. SEQ ID NO:563 has no apparent open reading frame. Expression of SEQ ID NO:563 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:564, 565); see Fig. 11. SEQ ID NO:563 is highly expressed in placenta. Compared to normal tissues, SEQ ID NO:563 is overexpressed in breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:563 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0234] The nucleotide sequence according to SEQ ID NO:566 was deduced from SEQ ID NO:149 and codes for a 155 aa protein (SEQ ID NO:567) of unknown function. The protein sequence is partially homologous to members of the tumor necrosis factor receptor superfamily and harbors a potential transmembrane domain. The protein encoded by SEQ ID NO:566 might represent a new member of the tumor necrosis factor receptor superfamily. Expression of SEQ ID NO:566 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:568, 569); see Fig. 12. Compared to normal tissues, SEQ ID NO:566 is overexpressed in gastric cancer, breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:566 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0235] The nucleotide sequence according to SEQ ID NO:570 was deduced from SEQ ID NO:53 and codes for a member of the kernel lipocain superfamily (SEQ ID NO:571). These secreted glycoproteins have distinct and essential roles in regulating an uterine environment suitable for pregnancy and in the timing and occurrence of the appropriate sequence of events in the fertilization process. Expression of SEQ ID NO:570 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:572, 573); see Fig. 13. SEQ ID NO:570 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:570 is overexpressed in ovarian cancer,

lung cancer and melanoma. Based on these expression results, SEQ ID NO:570 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0236] The nucleotide sequence according to SEQ ID NO:574 has no apparent open reading frame. Expression of SEQ ID NO:574 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:575, 576); see Fig. 14. SEQ ID NO:574 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:574 is overexpressed in lung cancer and melanoma. Based on these expression results, SEQ ID NO:574 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0237] The nucleotide sequence according to SEQ ID NO:577 was deduced from SEQ ID NO:20. SEQ ID NO:577 represents a partial cDNA with no apparent open reading frame. Expression of SEQ ID NO:577 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:578, 579); see Fig. 15. SEQ ID NO:577 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:577 is overexpressed in gastric cancer, breast cancer and lung cancer. Based on these expression results, SEQ ID NO:577 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0238] The nucleotide sequence according to SEQ ID NO:580 was deduced from SEQ ID NO:32. SEQ ID NO:580 represents a partial cDNA with no apparent open reading frame. Expression of SEQ ID NO:580 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:581, 582); see Fig. 16. SEQ ID NO:580 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:580 is overexpressed in ovarian cancer and lung cancer. Based on these expression results, SEQ ID NO:580 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0239] The nucleotide sequence according to SEQ ID NO:583 was deduced from SEQ ID NO:257 and codes for a member of the homeobox class of transcription factors (SEQ ID NO:584). Expression of these proteins is spatially and temporally regulated during embryonic development. Expression of SEQ ID NO:583 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:585, 586); see Fig. 17. SEQ ID NO:583 is highly expressed in placenta and prostate. Compared to other normal tissues, SEQ ID NO:583 is overexpressed in colon cancer, ovarian cancer and lung cancer. Based on these expression results, SEQ ID NO:583 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0240] The nucleotide sequence according to SEQ ID NO:587 was deduced from SEQ ID NO:148 and codes for a member of the IGF-II mRNA-binding protein (IMP) family (SEQ ID NO:588). It functions by binding to the 5' UTR of the insulin-like growth factor 2 (IGF2) mRNA and regulating IGF2 translation. Expression of SEQ ID NO:587 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:589, 590); see Fig. 18. Compared to normal tissues, SEQ ID NO:587 is overexpressed in lung cancer. Based on these expression results, SEQ ID NO:587 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for this particular tumor type.

[0241] The nucleotide sequence according to SEQ ID NO:591 was deduced from SEQ ID NO:194 and codes for a 372 aa protein (SEQ ID NO:592) of unknown function. Expression of SEQ ID NO:591 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:593, 594); see Fig. 19. SEQ ID NO:591 is highly expressed in testis. Compared to other normal tissues, SEQ ID NO:591 is overexpressed in breast cancer, colon cancer, ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:591 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0242] The nucleotide sequence according to SEQ ID NO:595 was deduced from SEQ ID NO:191 and codes for a 357 aa protein (SEQ ID NO:596) of unknown function. Expression of SEQ ID NO:595 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:597, 598); see Fig. 20. SEQ ID NO:595 is highly expressed in testis. Compared to other normal tissues, SEQ ID NO:595 is overexpressed in gastric cancer, colon cancer, ovarian cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:595 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0243] The nucleotide sequence according to SEQ ID NO:599 was deduced from SEQ ID NO:18 and has no apparent open reading frame. Expression of SEQ ID NO:599 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:600, 601); see Fig. 21. SEQ ID NO:599 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:599 is overexpressed in gastric cancer, breast cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:599 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0244] The nucleotide sequence according to SEQ ID NO:602 was deduced from SEQ ID NO:133 and codes for a member of the von Willebrand factor domain superfamily of extracellular matrix proteins (SEQ ID NO:603). Expression

of SEQ ID NO:602 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:604, 605); see Fig. 22. Compared to normal tissues, SEQ ID NO:602 is overexpressed in ovarian cancer and lung cancer. Based on these expression results, SEQ ID NO:602 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0245] The nucleotide sequence according to SEQ ID NO:606 was deduced from SEQ ID NO:128 and codes for a member of the Borg family of CDC42 effector proteins (SEQ ID NO:607). Borg family proteins contain a CRIB (Cdc42/Rac interactive-binding) domain. They bind to, and negatively regulate the function of CDC42. CDC42, a small Rho GTPase, regulates the formation of F-actin-containing structures through its interaction with the downstream effector proteins. Expression of SEQ ID NO:606 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:608, 609); see Fig. 23. Compared to normal tissues, SEQ ID NO:606 is overexpressed in gastric cancer, colon cancer and lung cancer. Based on these expression results, SEQ ID NO:606 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0246] The nucleotide sequence according to SEQ ID NO:610 was deduced from SEQ ID NO:118 and has no apparent open reading frame. Expression of SEQ ID NO:610 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:611, 612); see Fig. 24. Compared to normal tissues, SEQ ID NO:610 is overexpressed in gastric cancer, breast cancer and lung cancer. Based on these expression results, SEQ ID NO:610 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0247] The nucleotide sequence according to SEQ ID NO:613 was deduced from SEQ ID NO:116 and codes for a 76 aa protein (SEQ ID NO:614) of unknown function. Expression of SEQ ID NO:613 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:615, 616); see Fig. 25. SEQ ID NO:613 is highly expressed in placenta. Compared to other normal tissues, SEQ ID NO:613 is overexpressed in breast cancer, lung cancer and melanoma. Based on these expression results, SEQ ID NO:613 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0248] The nucleotide sequence according to SEQ ID NO:617 was deduced from SEQ ID NO:267. SEQ ID NO:617 represents a partial cDNA with no apparent open reading frame. Expression of SEQ ID NO:617 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:618, 619); see Fig. 26. SEQ ID NO:617 is highly expressed in placenta and endometrium. Compared to other normal tissues, SEQ ID NO:617 is overexpressed in lung cancer and melanoma. Based on these expression results, SEQ ID NO:617 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0249] The nucleotide sequence according to SEQ ID NO:620 was deduced from SEQ ID NO:182 and codes for a 829 aa protein (SEQ ID NO:621) harboring multiple putative transmembrane domains and a patched family domain. The transmembrane protein Patched is a receptor for the morphogene Sonic Hedgehog. This protein associates with the smoothened protein to transduce hedgehog signals. SEQ ID NO:620 might represent a novel member of the Patched family. Expression of SEQ ID NO:620 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:622, 623); see Fig. 27. SEQ ID NO:620 is highly expressed in lung. Compared to other normal tissues, SEQ ID NO:620 is overexpressed in ovarian cancer and melanoma. Based on these expression results, SEQ ID NO:620 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

[0250] The nucleotide sequence according to SEQ ID NO:624 was deduced from SEQ ID NO:184 and codes for a 323 aa protein (SEQ ID NO:625) similar to TWIK-related acid-sensitive K⁺ channel, a member of the superfamily of potassium channel proteins that contain two pore-forming P domains. Expression of SEQ ID NO:624 in normal and cancerous tissues was quantified by real-time RT-PCR using sequence-specific oligos (SEQ ID NO:626, 627); see Fig. 28. SEQ ID NO:624 is highly expressed in lung. Compared to other normal tissues, SEQ ID NO:624 is overexpressed in gastric cancer and lung cancer. Based on these expression results, SEQ ID NO:624 and its expression products qualify as molecular markers and/or target candidates for targeted therapies, in particular for these particular tumor types.

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 ttttctggaa tggaaaatta agttgttttag tgtttatggc tttgtgagat aaaactctcc 420

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 ccttctccag tcaccgcttc cgccagtacc tgaaggcttt cctggctgcc gtgcttggat 360
 45 ggcacctggc acctggcact gccaggcct cattatccag ctgttctgag agcagcatac 420
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ttaaagtcct ctcaccacag aagccggagt ttagtggtta ggggcacagg ttcttagata      180
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ctaa                                          304
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tttcagcacc caactgagat ccgaggagct cctgggaagc cctgggtgca ggacactggg      120
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cgagagccaa aggtccctcc ccagacatct ggacactggg catagatttc tcaagaagga      180
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 25 tattcaagggt tagtttcagg agcacag 567

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 45 cgaaggccca gaatccattt taggtttcca aacagacctt tcgtcccttc aagggtgaac 180
 caccgttttc cattccagcc attttattgg ccacaccgtt accttactta taggtatttc 240
 cccagaagaa gactccagag aggaagctca tctgaggaaa gctgagaggg aagagaaacc 300
 50 caaacatact gaagcaaaaa aaagcctatc cttcagaaaa aagcaacaaa aagatttctg 360
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gtcggaatcc tacacctgat cagaagagag aagatgatca ggtgcagct gagattcaag 360
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<213> Homo sapiens

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 5 tgcacacgtg gctggacgcg ctggggggcag gtccaggtca gcttcaagga ctctgcccag 360
 gctaacccta gaggcctcta gtgccagcag tta 393

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 10 <211> 493
 <212> DNA
 <213> Homo sapiens

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 gcaagacagt ttattttaaga gcattgcaat aggtaagtgc tatgggtctca atgttttgtgt 240
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 aaagaggcat tgggagagac ccctcacctt ttccatcata tgaggacaca gccaggaagc 420
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 40 tttgaatact gttgtgtctt aactgttat tacctatcca gtatctattt ccccatattc 240
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 <212> DNA
 <213> Homo sapiens

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<212> DNA
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cccaacttct gtgaatggac aagagatgca attgtgatca ctgaacatga ggcaacatct 300
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ttgaacaatc ctatatgaag cttacctgaa gttgctgtag ccgtttggca agtctgggga 420
gactaacaga cacactgagg atagcagaaa ataaagatag aaacagccca ggtttttggg 480
40 gaaattcatg agcttctgaa taacgaaccc cataccaccc tacctctata aaagaat 537

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ctcctcctga accctccaaa tttgtctaag aacttcgaaa actttaacaa acaggctgat 180

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	aggaagactg gcaggagatt tatggaaagg tctcttacia ggactcttga atacaagctc	240
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	tcaaaaggat aatgatttca taattttcta tttgaaaatg tgctgattct tggaaatgttt	420
	cattctccag atttatgaac attttttctt gagcaattgg taaagtatac ttttgtaaac	480
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	gtgggtccccg atttggaaaa cacttgctgt catattgccc catgcctgag aagacattca	240
	ccaccacccc aggaggggtg ctgctggaat ctggacgtcc caaagaaatg gtgtcaacct	300
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	cagagctgaa gaaaccactg tctgaagggc agccatcatt gaagaaaata atactttccc	420
	gcaaaaagag aagtggacgt cacagatttg atccattctg ttgtgaagta atttgtgacg	480
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 aagtagaaac acatcaaata tctatcagct gatgaaagaa taaacaaatg ggagtgatcc 180
 atacaattta atagaatcta gcacctaaaa aaataaaata ttgatactgt ctacaacaca 240
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 45 accaggntta gagataacat ttagaagatg atccagcatc tttacantc tgtgggttaa 180
 ggtggggcac ttaggggtag aatcaataac aatggttagaa atcaaattag acaagataac 240
 tgaaacagca tgatccatgt gtgactccaa gttataaagg aggacatgga ttaatggtat 300
 50 acttctaggc tataggggta gtacaagtgg aaggacacca tcttagcatc agatcacttt 360
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45 agaagtaa at caagcagcag caacaatagc agccactctc cgaagggtcaa ggaagacctg      180
ccccacacag nccctcatc ctgcatcatg gacaagaacg cagcacttca gaatgggatc      240
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50 cgtcgcttcc acagggggccc ctcaagagct gtgactcggg agagctacct tactttgacc      360
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cccagaggct cctcagctgc ctgccagatg tggaaagggc cagctgacg cttctcctgg 240
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ccgtgtgctt cgggcctgtg ctgctgccgg cagccagggc gccacaagg cctcgtgccc 360
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gccaggctgc tacaatcccc gcctgccccg acaatctcca gatgtcgcgc cttacttgcg 540
acc 543

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acaccaccac ccccatccag agcatgatgt gccagtacct ggccagagtc ctgggtggagg 240
acgatgagat catgcaggga ttcacaggg ctttcaggcc cctgcccagg cacctatggt 300

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acttgctgga cttgaaacag atggaagagc cgtgccgttt ctagctcacc tccgcctcca 360
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5 catcttctct tcttattgta aatgcttctc ctgggttaac ttgtaccaga ataacctgtt     180
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40 cgggccatct gctcactctg ntcgcgcgcc acgacctggc acttgtggga gatggtctgc     180
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 aacaatgaca caatctctag agagacatag gtgttcggcc tggctcaatc actagcctta 180
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 agcagcggcc ggatgcctcg gaggaggaca gcttccagtg gatgagccgt gtgctgcagg 180
 tgggcgcccc ggcacggcct atgggttcggt gaatctccca agctggcacc cccactccac 240
 tccaagtgcc aagtggttgg cttgtcccg cgggtcctcc ctgggtccag ctttgtttat 300
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 tgtgtgccaa acaatattaa aaattgctgt atatacatgt ttgccattta ttatttataa 180
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55

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 atcaccacaga ctggctgctc tgactttcaa gtgcctggga gatcagtgcc cagtgtactg 240
 ccgagtgata cgtgaaaaga acctatgtca ggacatgccc tggatcagc gctgctgtga 300
 aacatgcagg gacttctatg cccaaaagct gcagcagaag agttgacctc tagcaggctg 360
 gctggatcac agctcttngc aattacatta tttataaaca cacacactag catgtttttc 420
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<400> 67
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 aagcttcccta agctgctggc ctgataatgt gtataaatat gtatgcaagt atgtatatcc 240
 ctatagtatt tatctactta ggatataaga tataatctcc tgattatgct ttcaatttat 300
 tgtcttgctt cattaaaatg taaggctaag gagagcatgg aatttgtcag ttttggtcac 360
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 <211> 291
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 actccctttc ctctggagt tgagaagccc ccacagagac tggctatggg ggagtgactg 180
 tctatagggt ccttggtatg cctgcctatc tgcaaatga gaatgagatc gataccttca 240

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291

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 aatcaaagtc tcttgacctt gggtagacac gctaagattt gtacctagag atttctgagt 180
 35
 gttgacttct ctctgcccc cacctatctc cccccccna aaaaaaaca caacaacaac 240
 aacaacagaa cataccaggg attcatggct tgcccaatgt tggaggggga gaagagagga 300
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 10 cccattcagg tgtcttttag aacattatctt anccactaaa tatttatata gttgacataa 180
 tgcttattat gcccttgaat aatagaattt gttttgtttt tacttcttat ccataagcat 240
 tggccttaca ttgcctcaag aggaacagaa tttattatta aacaggattc ttaaateccat 300
 15 aactcatatt gtgacttcat acattttgta accctagtag tgaatatacc ct 352

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 25 gcctgccagg acgcgacgca gctgctgagc cacgggcagc gcatgctggc ggctgtgggc 180
 gcggcgggtgc agcacgtgga caacctgcgc gccgcgctga gcccgctggc ggacctgcac 240
 gcgctcgtgc tgcgcgtgga cccagccaac tttccgctgc taatccagtg tttccacgtc 300
 30 gtgctggcct cccacctgca ggacgagttc accgtgcaaa tgcaagcggc gtgggacaag 360
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 cgtnggcatg aaatcctnng gggctgcttt agaaattggt ttctttggct gctgggtgggg 180
 gtgctgctgg tggggggttg cacagctnng canactgcan ccagtctggt ggggggttgc 240
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 ctggcttttg agaagttggg gctctgaagt gggaacacaa ggctgccttt tgcaggntca 360
 ggtgtaaaatt ctccccctgc cactttcagc ctacgctgaa acagatggag tgtgcattcc 420
 cacttcctt tatggtaccc tggaatgatg gagctgcca gggcatcgcc acgttactct 480

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ctgccgcccc tgccctcaggt ggtgtgcacc taccgtgatg tgcgcttcga gtccatccgg 240

ctccctggct gcccgcggtg nggtggacccc gtggtctcct tccctgtggc tctcagctgt 300

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<210> 75

<211> 275

<212> DNA

<213> Homo sapiens

<400> 75

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tcttaggatc atcaaaagaa aaagaggatt tggattatgc aaaaaatgat tcctatatat 180

ataatcaatt atctaactga catttttgca aatctaccac aacttcgcct tttattgcat 240

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<210> 76

<211> 62

<212> DNA

<213> Homo sapiens

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tt 62

<210> 77

<211> 471

<212> DNA

<213> Homo sapiens

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tcgggacaaa tacagaatgt gaggtcccat tccagccctg gaaactggac acagcagtag 240

ggcggacgca tcaagtgata aatgaccctg tcccctttgt tcgctgtact ctctggcaa 300

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aatcaatcta aatactgctt tgcaaagtaa aaaaggaatc aaaatgacac ataagacaat 300
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cacata 366

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<212> DNA
<213> Homo sapiens

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<400> 81
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<210> 82
<211> 119
<212> DNA
<213> Homo sapiens

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<210> 83
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<212> DNA
<213> Homo sapiens

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55

<400> 83
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cagagtgttc ttggtgc 137

5

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gcctaggatt ttaggggtcat cagccaaaaa tggaactgcc ttctagaaca aaaaatgaca 180
15 tctttttgag gaagacagtc atccagagtc ttacaatct tttaccaca ttgcctagta 240
cataattaaa catttctaga tatgaatagg aacaggaaaa tgtgacccat aatcaagaca 300
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<210> 85
<211> 459
<212> DNA
<213> Homo sapiens

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tgccacactc ttcacatttg taaggtttct ctccagtatg aattatctta tgtttattca 180
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tatgaattct cttatgttca ttaagggttg tgaaccgact aaaggctttt ccacattctt 300
cacatgtgta gggtttctct ccagtatgaa tactcttatg tttattaagg gttgcggatt 360
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<400> 86

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      catggagttt aaggggttat tatggctgag atccagacca tgagcagaga aaagttcagt      180
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      ccctaaaata attttagaca aattgtaaaa cctagttaaa gacatatatg ctgatatttt      180
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25      taatggatgg aaataggagg agagaaatgg atcgatgtgt aaataaaaca aatctatcta      300
      aatgttaaag cttaattgta gatgatgaat gtaggagtgt tgaatgttaa a      351

30      <210> 88
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40      aacccacaca caaccacgc acaaataatt ttgggggggc ctcccatggg cattttataat      240
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      agcccaacaa agaacttctt tgacattttt tagtgtaaag gtaactgacg gtatctacca      360
45      aattagcaat ttgtaaaact ggaatttcta aaagcaaata cttggagctg agattacctc      420
      ccacttccca aattcgagtt atatgatctc aagtataata ccctttggta tagacctagc      480
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ctagccaccn caaancactg tcatagatgc agcaatccac tttcacaaaa ccccatggac 180
aatgcagagg gggagaacag ggactgatta aagaaaggga cagaaatggc atcactatcc 240
25 aagactgaaa aacaggctga atggattatc actctgacct aactgcacat ttctaattgc 300
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45 tcttcccccta ttatttgcct cctggaaaac ccaggacct cttccccatc tccanccct 180
accctgggg gcagcccagg gagagccagg cacaatgagg gctcccaaca gctgcaagga 240
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 20 tacctccctt tttcccttct tctcctctca cagagctgaa gaatattttg caaagttcat 420
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 35 cagctgcaga gcaggaggct ccccggtgcc tctcttctc aagcaagtca ggatcccaag 180
 aggcgcgtgc ggggaggccc ctccgaaggg ctgctggctt gtgtcttcca ccagcgcaaa 240
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 40 gaggtgtcgc tgtcggg 317

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 5 gaagatacag ttgttcatat ggaagcaa 208

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 50 ttttatgcac ataaaagatt tcttttaggga ttattgtaca gagttctagn aaaatatata 180
 attttttttt ctgggcttat aactttcttt tctaaaaatt tatttggcag cctgattaga 240
 aatgtggtaa aatctgaaca ataaaatagn aaatagacta gttgcataga atgtttcaaa 300
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 5 aagaatttca ttgacattaa tgacactgta tacaataaat gtgtagtttc ttaatcgac 360
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 tttttaacct gccacctagt ggccgaaatg ttgctatact attgataagg tactcctaata 240
 tttggcaaaa tagtaagagg caaagcacca aagattatgt tctctccctt ctccaaatct 300

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5 aaagttttga ttttaattgtt tccttttagc ttatttttga gatatgcagt ctgttaggaa 480
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tataagaata aagcgacttg cttgatatgt acagtagata ggtacagctg tagctgctgg 180
ccatttcaga cagatgcttc atcttgtaaa cagcaacata aatgtatggg accaataaat 240
20 acagtacagt actgtaaatg tgttttctct tccttatgat tttcttggtg catgttcttt 300
tctctagttt actttattgt taagaatata ctatataata cacatacaaa atatgtgtta 360
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35 ctttgccctc gaagaccagt gtcagcaagg tgggtggtggg tgggctgctc ccatccgtcc 180
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 ctaacatcat gatatactgg aaacaggtat ctctttcctt tacccttggtg cctgctgang 360
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 gatacattat ggaggcagaa gtgttcattc aacaagcgtt tgtaaataat ctactatgta 180
 atcatgatta tacaactaga gagaatatga aaaaaatgaa ttacgtatgt tagcttatag 240
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aactgtatca aaggagaaaa agggaaatac aggcttatcc taacaatttc acagtgaaca 360
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25 tgcaaaggcc aaggggtgga gcagcccagc atgttctgga aaaggtaggg ctccccaagg 240
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50	gccagcaggt cccagcttt ggctatgagg gccttgagtc ccccaaaaca ccgggttcca	240
	gcaccacact cagccctcat tggctcttga actgagcttg gaagcttctg gtgaccttcc	300
	aagagcctga gagtgaggtg gaattatttt aaaagataaa tattatatta tatatatata	360
55	tatttccctg aaggaaccaa agcgaatttt aaaagatgca atgtagaggg gaaaagagat	420

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ctaagaatat t 491

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15 aattgagtgg gctgtggagc cgaatttcac acctggtact gccagtccag ccaatcttag 240
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<213> Homo sapiens

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30 tgtggacttc agcgatgtgg gctggaatga ctggattgtg gccccaccag gctaccaggc 240
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<211> 494
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 tcccaagatg tcagaataag actccccatc atgatgaggc tctcacccct cttagctgtc 180
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 tttacataac atctcaggag gaaatgtggc tctctccatc ttgcatacag ggctcccaat 360
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 15 aggaaagctg aaattatagt agagtcccct ttaaattgcac attgtgtgga tggctctcac 480
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 <223> n is a, c, g, t or u

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 30 <222> (235)..(235)
 <223> n is a, c, g, t or u

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 40 acggcaacca gtaaaatgac tatttttact gtcttatcta ttaatgaaga ggagattgca 360
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 atctaategc agt 553

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55 <400> 119

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45 gttctcttgt ggtaccacag gctgtaacca gtccaccag tgttgtttta gaaattttaa 480
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<211> 326
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 gcgcagccag aaccgctcca agacgccccaa gaaccaggaa gccctgcgga tggccaacgt 180
 ggcagagaac agcagcagcg accagaggca ggccctgtaag aagcacgagc tgtatgtcag 240
 cttccgagac ctgggctggc aggactggat catcgcgcct gaaggctacg ccgcctacta 300
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 gtgtgtttct ttgtttttta tgagaaaatt agtcacagaa tttaagatct tagttacttc 180
 tataggggaag gcaggggaat gggacaagga ggaagccac agcattgggc atgctctcat 240
 gttgaagttg ggttcaaagg tgttcattat taaaatgctt cataatgatg accatacatt 300
 25 tggatattct aggacaatct tgggttacat ctattgtctc aacataatta ttcagtgcaa 360
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45 <210> 124
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 gcctgtccct ccagatagtg ctctgtttct ctctgtgtgc cccctgcctg gtccctctggg 240
 55 gccactgtgc tttctgctgt gtgcatttat aaatgatgtg tattttatat agacctgctt 300

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ctatggcctt agcctttga 379

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<211> 495
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15 acttggtgctg gaggttaagat gccactagg cagcccaccc agagggcaag atggagaaca 240
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20 tttgttttca acctcatgta atttgtgcag atttgttggt aaaatacatc ttggcacaat 420
gagtgtctct gctgggtgctt ctccaagac tatcttgaag gtgggctggt tgcctttcgt 480
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35 cacaggcacg tatatgccga cggctgcagc tatgcaagga gcttacatct cccagtacac 180
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40 ttccccctccc catctttact gaatagaaat gaattcttgg agatactcat gctcccagat 360
tccagagggg taaccaggaa tggagaccat ccgtcgcccc tgctaaggac taacacttag 420
ccatcgtttt tcacaggcct gggcctggaa aaagaaatct ctacgttcct gccctttact 480
45 attgctgatg g 491

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 aagcccccca caccttttcc ccaaccacag agaacaagag tttgttctgt tctggggggac 300
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<210> 128
 <211> 458
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 20 tcagcccagg cgccctgagc atcttggggc acctggaccc catcacaata ctcttctctc 180
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<223> n is a, c, g, t or u

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agctcagctg cctctttctt gaggacaccc tactgatca cccagacca gccagagtgg      240
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<211> 414

<212> DNA

<213> Homo sapiens

<400> 131

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ttgtggcaat ttgttacagc agcaatagga aactactaca ctgtgtctga ttagatcagg      360
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<210> 132

<211> 408

<212> DNA

<213> Homo sapiens

<400> 132

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gctaaatctg atcctcagcc cactctcaga atcgataaat gcccttaggt gattgtgaagc      180
tcacctaaaga tataacttttt ctctctaga attttagttt attagatttt tctagttgtc      240
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 actgtccttg ctcatgcctg cctctttcac ttggcaggat aatgcagtca ttagaatttc 240
 acatgtagta gcttctgaga gtaacaacag agtgtcagat atgtcatctc aacctcaaac 300
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 <211> 479
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<220>
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 <222> (305)..(305)
 <223> n is a, c, g, t or u

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 ggtggagggg ctggaggagc aggaatctct cttgttgata ggtatgaggc cttgaagtcc 180
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 cccctaagtc aggcctctcc tcagttacca gggctctcgt cagagccctt ggagcctgag 300
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gataacttcc atttggtaca caacttattg tacatagagc tatgatttga ggaggcatct 240
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gggaagcact gaatatgatg gggctgtatg atgggatgga gcacctcatt tatggggagc 180
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 tgctgagcta gccaggactg atggagcccc tgggggtgtg ggatggagga gggTctgcag 180
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 50 ggaaatccat tccattttgt gaattgtgac ataataatag cagtggnaaa agtatttgct 420
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 catgagagta gccagcaaga gcagggccac agcccagaag gatgagaaat gctacgaggt 180
 gttcagcttg tcacagtcca gtcaaaggcc caactgcgat tgtccacett gtgtcttcag 240
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 gcagccatct cactttcttg atatttctga ggattgggtct cttcacacag atgatatgat 360
 tgggtccatg tgatcctcag gtttggggtc tcctgaagat gctatttcta gaattagtat 420
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 ctactagaa cactggcatt ggagctggcc cccaaggaca tccgggtaaa ctgcgtgggt 180
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 gtgtccttcc tgtgctctcc agatgccagc tacgtcaacg gggagaacat tgcgggtggca 360
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   ggctntgaa cttccacctc ctggggcctc ccagacctcc tgtgccccca cctgtgtggg 180
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40 cccagcacgc ggggtccac tgtccactgg aggttctggc tgagcccagc accccggact 300
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 gcctccaga gtgctaggat tacaggcatg agccactgca cccagcctct taacaaatct 420
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5 gatattacta ggttttacgt tgcattctcca gtattgatct ttggaaactg atgttacatt 420
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 cgcccaccac nnnnccccn tnnttcctgc tgctaccct gtgtcccag ggctgggagt 480
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 tctggcggga caaggatgta accatcaagt gtggcattga ggagaccctc gactccaagg 180

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5  tgccttcctt gccggcgctg gttggccagg tcctgctcat ggctgacttc aacaaggaca      360
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40  tgcctaacat ccaggccgta ctgctcccca agaagactga gagccaccac aaagctaagg      180
    gcaagtaagg gctgaacttt aaaaatgtaa acttacaaga caaaaggctc ttttcagagc      240
    caccaccat ttctacggaa gaactgagca ctctgttctc caaacctatc agaaatttgt      300
45  ggccgagttc aagcactgag gccattactt tcctattggg taaaataaaa gtattgaatc      360
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acaggtgaag cagcaggagc agaaataccc tcaggagtc gcctcacagc gcagcaagtg 420
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tgacatctct cccnttgaag agcagtcaga ctctctgctt gctcttcaga cttaatttgg 180

gggtttaaca ggtgaggttg ctgggggaac tctttttacaa catctctctg aaagaatccg 240

ggctgccagt ttcatttggg ttgggtgtca gtagcatgat ggaaagacaa aaaaacacaa 300

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gttcagcaat t 371

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gctttttcga cgtgtggcgt cggctctacc cggaatggag aatgtccagg agaaaagcaa 180

agaagggatg attgacatca agctggacaa accccaggag ccccgccca gcgagggcgg 240

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ggctgcccct cctaccacct acctcattct gcctactcac cccaggggcc acagccacag 180

cctgctggac tcaggactgt cctgtcaact ccagacaact gaataaacag gccgggtaca 240

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cttagtttca gacatgtcag aagcagctat atagcatatc ttattctatg atatacatca 240
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taagagatta cgttgaagaa cgatctggcg aggatccact ggtaaagggc atcccagagg 180
acaaaaatcc cttcaaggag ctcaaaggag gctgtgtgat ttcataatac aaacaaaaag 240
aaaaaaaaatt aaacaaattc ttggaaatat ctcaaatgtt aataacaata tgaatttttc 300
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ggactgcggg acgatcctcc tccaagacaa acagcggaaa atctactgag tggcttgtca 180
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gacagccctc ttgcagaagc tgacctgggc ctctgctgaa ctgggctcca gcacctccct 480
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 aatggccaga tggattgcac gaaacctgac ttggattcac catcttcc 408

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 ttaatgagaa cctggtcatt gggaaagccc caagcctgcg tcttgctgtg atgccttccc 180
 cattatgaag ggtccattgg catgggagtg gggagacctg gactcanana agctacaagg 240
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 tcagcagaca gcccataacc aagagccaag g 331

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 5 taaacaaatt gctctaaatg gcctcagtat caagggtgtgc tttctgtacc cttaatctga 180
 ctttaatcct gcagaacctc agtcttacca tgtttaacag cattgccatg tacgatatgc 240
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 30 gncaatatct tattcttctt tccttttaaa tacttactgt ttcaatttca aataaaaaaat 180
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 atacagagct atgtaataat aactaatttt aaatcctgac aaattagaag ttaagcctac 480
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cattttatat atggaggaac tctggacatt ccagacaaaa ctaatgttgg tcagatactc 180

aatatggctg atatgtatgg actagaagga ttaaaagaag tagcaatcta tattttaaga 240

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tgctgatta ttgctcattc agttggagtg gaaagtcttt ttgctgactg catgaagtgg 360

attgtaaagc attttgcaag gttttggtct gagagaagct ttgcaaatat acctcctgag 420

attcagaaaa gttgtcttaa tatgttgatt cagtccttan tnnnnntnnc nngannnnnn 480

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<212> DNA
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<223> n is a, c, g, t or u

<400> 181
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ttcaagaaag accttctaaa tttatattag gacatagtga gaagaaagcc atctgaaaac 120
caggaagaga gccctcacca gaatctgacc atgctgggtgc cctgatnctt ggactttcag 180
cctccagaac tgcaaaattc tgggtgtgggtg tgaatgctgt ggctcagtcc gaacatgttt 240
ttttctgtaa ttttatcatt attacacgat tgcaatatca gttttgtttt ttaattggaa 300
agcaacattt tctactgttg aaagacgttt tttgacaaat 340

<210> 182
<211> 416
<212> DNA
<213> Homo sapiens

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<400> 182
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 tcctgacttt tttcctagtg atccaccctc tgggaaactt ctggctaatt cttagcgtca 120
 5 cctcaattga gctgggcgtt ctgggcttaa tgacattatg gaacgtcgac atggattgca 180
 tttctatctt gtgccttata tacaccttga atttcgccat tgaccactgt gcaccactgc 240
 ttttcacatt tgtattagca actgagcaca cccgaacaca atgtataaaa agctccttgc 300
 10 aagaccatgg gacagccatt ttgcaaaatg ttacttcttt tcttattggg ttagtcccc 360
 ttctatttgt gccttcgaac ctgaccttca cactgttcaa atgcttgctg ctact 416

 <210> 183
 <211> 503
 <212> DNA
 <213> Homo sapiens

 <220>
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 <222> (78)..(78)
 <223> n is a, c, g, t or u

 <220>
 <221> misc_feature
 <222> (84)..(84)
 <223> n is a, c, g, t or u

 <220>
 <221> misc_feature
 <222> (210)..(210)
 <223> n is a, c, g, t or u

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 <221> misc_feature
 <222> (247)..(247)
 <223> n is a, c, g, t or u

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 <221> misc_feature
 <222> (371)..(371)
 <223> n is a, c, g, t or u

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 ccaccctggc cccgagtngc cgtntgctgg gcctttcctt cctggctctg caccatgc 120
 45 tggctgcccg gtctggcttc ccttcttgct tctgtcttgg gcgaggcagc tgtgagcatt 180
 gcacagaggc aaagaccctc ctgcagcctn tgcgctgggc cgtagaaaca agagcctttg 240
 taatacngaa cctcattcaa ggattaggag tgggtggttag gtcagggcca cccccagtgc 300
 tgcaggaacg gcctccaccc agctctgttg gtcagagcct gggtcatgca cctggagtgt 360
 50 ggagatcaag ntgggtctca gggcagttag gtggccatat ccaccacatc gcatttctgt 420
 ggggaagagg tgacctcttt gttttaaact taagggtgtc gcttatccag ccagaaataa 480

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aaatctgccca gtggtgttcc caa

503

5
 <210> 184
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 <213> Homo sapiens

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 <223> n is a, c, g, t or u

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 <220>
 <221> misc_feature
 <222> (294)..(294)
 <223> n is a, c, g, t or u

<400> 184
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 gaaggggtcct gtccctgtcag tcccagaggga gccacaacca aagctgcgga gagaagggtgg 180
 ggaaggggtgc ggaatggccg tggggcacag cgtggcagac tgttcagtct ctgctgggtc 240
 25 tttcctaggg acctggaagg ccagtgttgc tccccctca ctccctttca ctgnaggcag 300
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 tgggtgacca tgccctc 377

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 <210> 185
 <211> 390
 <212> DNA
 <213> Homo sapiens

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 <400> 185
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 cgcagaaagc ccgactcctc cttcagtccc tcctgagcta ggtccagcag cctgaggaag 180
 40 cgaggggtcgt cgtactcgaa gcggcgcccg caggtgaggg aggcgatcac gttgctcacg 240
 gctttgtcca agagaccgtt ggggcgaaaag gggcgctcga gtggttggtg aaggcggcac 300
 aaaggcaggc ggcctcctcg gtcacccact gctccagcga cttcttgccc aggcccaagt 360
 45 tgcgcaagggt ggagacggag aagcgctct 390

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 <210> 186
 <211> 188
 <212> DNA
 <213> Homo sapiens

<400> 186
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55

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ctcagggagg cactactggg aggtggacgt ggaaaaggca accaggtggc aagtgggcat 120
 ataccacggc tctgcagacg cgaagggcag cacggccaga gcttccggag agaaagtctt 180
 5 gctcacgg 188

<210> 187
 <211> 549
 <212> DNA
 10 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (213)..(213)
 15 <223> n is a, c, g, t or u

<400> 187
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 cagctctgga gacgcagaat tccacatgag gaatgtggaa ttcagcatgg ggatgacgct 120
 20 gcttcaccca gacttggagg agcgtggtga attgcccgtg cccatgctct gatgtgcctc 180
 tctggccgct gcgttctctc tttctccctg ccntgggtca gtgcctgtaa aactgcctc 240
 aaatcagcag ggcccccgct acttctgctt tatgcacctt tttctcaga cacattaata 300
 25 caggggagtt ttgtttccaa gggaccacat ccagatggag gggctgtttt tggatgatctg 360
 cactgccaaa tgcccagagt tccctgacag tcggagctga tgaggccaag gctgtgtgtg 420
 gttcctcttg atggccagaa gaggaaccaa aacactgaat tctgggcctt cttaagagtg 480
 30 gtgatcagca cattgtgata gaagcatatc tgggaatgaa cttggcctca agcttttggc 540
 cttttaatt 549

<210> 188
 35 <211> 459
 <212> DNA
 <213> Homo sapiens

<220>
 40 <221> misc_feature
 <222> (120)..(120)
 <223> n is a, c, g, t or u

<400> 188
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 tgtcctgtgg gatgacaagg caggtccaaa cctttgcctg ctctcccatc cattcctttt 180
 50 gtgttagtcc atgtgtctcc cgactgttct ctccaacaac aacacagact gacaaaacct 240
 actgacttgg agtcaggaac agactttgct attttctggc tgtgtgatcc tgatgagtcc 300
 cttgaacctc ctggacttgt tcctcagcct aaaaaccaag actaataaat caagtctatc 360

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tcacagcctt acgtggggat caaaaaacat ggagcatgtg aacacacatt gtacatcacg 420
aagctgtgtg caaataaata tcgtgtaact ccagccctt 459

5
<210> 189
<211> 430
<212> DNA
<213> Homo sapiens

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<221> misc_feature
<222> (112)..(112)
<223> n is a, c, g, t or u

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cacgccccca agactccttt gtcgccccag gggcgggacc tgagctgtcg gtttcaggag 180
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cccttcgtga cttcaaaagt cctgggcact gttgctcatg agtgctgcac aactgtcgcc 240
ctctaaagcc acctccatcc ctcaactggc tggcctcctg agccttcggt gaggaaacgg 300
ggttccgagt tgcccgcctg agagcttaac agtctgacta gaaaagggct aattcgcttt 360
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ctgtgcaaat ctcttgagct aattatttaa tctgaaacat ggacaggtaa aggaccattg 420
gcgggcgtgg 430

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<210> 190
<211> 406
<212> DNA
<213> Homo sapiens

<400> 190
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cagatgctaa ggtgaggatg gtgatgatcg ctggatcacc agaggctcgg ttcaaggctc 120
agggagaagt tatggaaaaa tgaaagaaga aaacttcgtt agtcctaaag aagaggtgaa 180
40
acttgaagct catatcagag tgccatcctt tgctgctggc agttactgga aaaggaggca 240
aaacggtgaa tgaacttcag aatttgtcaa gtgcagaagt tgttgcctt tgtgaccaga 300
cacctgatga gaatgaccaa gtggtgtca aaataactgg tcacttctat gcttgccagg 360
45
ttgcccagag aaaaattcag gaaattctga ctcaggtaaa gcagca 406

50
<210> 191
<211> 555
<212> DNA
<213> Homo sapiens

<400> 191
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ggcaggcccc tgtcctcctt caaacataca gggaaatcctg gaatggagaa aacatagaat 120

55

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	cagtgaaca aagccgtagt ccagtttctg tgttttctg ggacaatgaa aagaatgaca	180
	aggactcctg gagtcaactt ttcactgaag attctcaagg ccagcgggtc attgcccaca	240
5	acactagagc tccttttcaa gatgtaacca ataactggaa ttgggactta gggccgtttc	300
	ctaacagtcc ttgggctcag tgccaggagg atgggccaac tcaaaatctg aagcctgatt	360
	tgctctttac ccaggactct gaaggtaatc aagttatcag acaccaatc taaatgtttg	420
10	aagctttgtt tctaaaagta ccttgaaatg atagagatgt aggaaaatat agttgtgggt	480
	ggagagagga gtgagtttgt ttaggtggga aggtggcatg ggatgaagtt gtcattactg	540
	agcatcttct ctgtg	555
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	cggagctgct tctgctccct ggggcatatg gactgacca cctcctgctg agaaccttcc	180
25	cctaggccct gtgcagaagg gctactgccc cttaggcctc agctggggga aaggcagttc	240
	tggtgctgta gaggccttg tgcagaaagt gggacgtctt ttttcctaag gtgtttaagc	300
	acaggcttga taagtttggt ttttaaaaaa taatctagga aatgaataat tctaaatcta	360
30	gtaatgagga aactgagcat ttcttttgcc ctccagggtg ccaagaccct acatatgaca	420
	gaacccttg ccttctcca tgcctgtggg atctgtttct ttaaagcact ttgtactgtt	480
	attcaggagg ttgataatct ccttgaccca tgtctttcta cctaataccc cacttccctg	540
35	cagaatcaat ctga	554
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	aggcgctcgc cagcctcggc gcctggactc gagccattgt cgccttctag ggacccccga	180
	gggcacaggg acccggggccc ccgcggggct ggggcccagac aaagactcgg caaaggggcg	240
50	agaggagggga acgagcgggc gccggggccac tcggggctga gctgggggag agcgggggca	300
	ggcggctgat gttttataa	319
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<210> 194
 <211> 218
 <212> DNA
 <213> Homo sapiens

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 cctgttgaag ccctgaaaca aatgttattt aaccttcaag cagtacaaga acgttttaat 120
 10 caaaataaga ccacagatcc aaaagaagag attaaacaag tttcagaaga tgatttctct 180
 aaattacagt tgaaggaaag tatgattcct attactag 218

15

<210> 195
 <211> 246
 <212> DNA
 <213> Homo sapiens

20

<400> 195
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 tcaggttgcc agacctgtca cacagtgggc tctgataggg ttacggaggg ggcctggctc 180
 tcagtctcta ctctcctatg tcccatcagt tgggtggagg ccaccttcca ggggggatgg 240
 25 gagaca 246

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<210> 196
 <211> 283
 <212> DNA
 <213> Homo sapiens

35

<400> 196
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 cacagtaact aaaagcaatg gagcagtgtc gataaaagta ccctacaaat taggacttag 180
 ttttaactatt attgcttaca aagatggcta cgtgttgacc cctctgcctt ggaaaaccag 240
 40 aagaatgcc aatatattcat cagttacact ttcactgttc ccg 283

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<210> 197
 <211> 391
 <212> DNA
 <213> Homo sapiens

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<400> 197
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 cagccacca cctacctcc cccactcccc ctctgacagc cagtggggcc accacagctg 180
 ccaacggggg tagcttgaac tgctgcaga caccatcctc caccagcagg gggcgcaaga 240
 55 tgactgtcaa cggcgctccc gtgccccct taacttgagg ccagggaccc tctcccttct 300

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tccagccaag cctctccact ccttccactt tttctggggc cttttttcca cctctttctac 360
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<210> 198
<211> 563
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<213> Homo sapiens

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<222> (116)..(116)
<223> n is a, c, g, t or u

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<221> misc_feature
<222> (165)..(165)
<223> n is a, c, g, t or u

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<220>
<221> misc_feature
<222> (168)..(168)
<223> n is a, c, g, t or u

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<221> misc_feature
<222> (175)..(175)
<223> n is a, c, g, t or u

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<220>
<221> misc_feature
<222> (225)..(225)
<223> n is a, c, g, t or u

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cagcctccga gagggagaga gagagagaga ggacagcttg agccggggccc ctgggnnttg 120
35 cctgctgtga ttccactaca cctggctgag gttctctctgc ctgcncnngc ccccnagtcc 180
ccacccctgc cccagcccc ggggtgagtc cattctccca ggtanccagc tgcgcttgct 240
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40 aaagggtgagt ttgagctgcc ttccctagct ttagaccctg ggtgggctct gtgcagtcac 360
tggagggtga agccaagtgg ggtgctggga ggaggagag gaggtcact ggaaagggga 420
gagcctgctg gcaccaccg tggaggagga aggcaagagg ggtggaggg gtgtggcagt 480
45 ggttttggca aacgctaaag agcccttgcc tccccatttc ccatctgcac cccttctctc 540
ctccccaaat caatacacta gtt 563

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<210> 199
<211> 591
<212> DNA
<213> Homo sapiens

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<220>
 <221> misc_feature
 <222> (60)..(84)
 <223> n is a, c, g, t or u

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<220>
 <221> misc_feature
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 <223> n is a, c, g, t or u

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<220>
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 <222> (182)..(200)
 <223> n is a, c, g, t or u

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 <222> (453)..(478)
 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 cnnnnnnnnn nnnnnnnnnn nnnnnntgga tattggtgcc ctcaagccag gtggacggca 180
 annnnnnnnn nnnnnnnnnn gagcacgaga gctttgagaa gcctcagctg ctgactgtga 240
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 ttggccagaa tgaggccacc ctgacctgcg atgctcgcag caaccagag cccacaggct 360
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 tcctgatccg tcctgtggac aaaccaatca acnnnnnnnn nnnnnnnnnn nnnnnnnntg 480
 ccctaggagc tcgcnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnagcn 540
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45

<210> 200
 <211> 485
 <212> DNA
 <213> Homo sapiens

50

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 agctattgag gagtctttac agcaaattaa gattcagatg ccttgctaag tctagagttc 180

55

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tagagttatg tttcagaaaag tctaagaaaac ccacctcttg agaggtcagt aaagaggact 240

taatatttca tatctacaaa atgaccacag gattggatac agaacgagag ttatcctgga 300

5 taactcagag ctgagtactg ctccaggggtg gtgtgcaatc ttatatgtat gcttgtgaat 360

ctgccatttg atttgtagga taaataaata tgtttaatat taacaacttc catcaaaact 420

ataataataa tattatatct actgttgacc tctaacaaca atcagggtgct gtattcagag 480

10 tcata 485

<210> 201

<211> 432

<212> DNA

15 <213> Homo sapiens

<400> 201

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taggaccagg ccatecttgg ctccagagct cgaagacccc aagacagccc tctgctctca 120

20 gcggcgccac agagagcctg ggctcagcct tctgcatcag gacatggcct cgtccactga 180

gggcacgatt taaacatttg acatcagaag ctttatttgt aaacctcaca cagataagga 240

ccaagggtcg gcggtgtggc cagaggacag ggggaagctga agggcccgtg cttgagctcg 300

25 gcagtcctgc tccttgacgt gaagccacca tgggtgaccg tccagcctca cccggtggcc 360

tgcacagtga gggaagggtc tcagggccat ctgctcccag ggcaggggac aggccaccaa 420

ggaccttttg ca 432

30

<210> 202

<211> 499

<212> DNA

<213> Homo sapiens

35

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<221> misc_feature

<222> (425)..(425)

<223> n is a, c, g, t or u

40

<400> 202

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caagtacgag gcgctgcaga ccttcgcgcg caccgtggcc cggggacctg tggcgccctc 120

45 caaggtggcc accaccagcg tcatcacctat cgtcaagtcc accgagctct cctccacctc 180

cgtgcccttc tcggctgcat cctagtgcg gccgggggcg gggggtggcg ggcggcgggc 240

ggcgggcagg cgggtggggg cacaccctc gtacctgtca ctgggatgca gactctcgac 300

50 atccgagtcc aagcgcaggc ccctcgggcg caggcagctc acaccaggaa gagactgtat 360

tgcaggggtga agagtgggct cccgtgggac cagagctgca cgccggtcca cagacacact 420

cacgnccgcc acctgtctcc cgcagatgtg tctgtgtgtg ggaattggta tcttgcaccc 480

55

gtgggagtcg ggacatata

499

<210> 203
 <211> 569
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (107)..(107)
 <223> n is a, c, g, t or u

<400> 203
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 cttatgccaa taccctactc catctattac tgcagtgtat gataagtctt gaaatctagt 180
 agtgtaagtt cttcaacggt gcccttaatt tttaaaatca ctcttgctat ttaaaattgt 240
 ttgtattaca tggaaatttt ataatcagct tgccaatttc taaaaagtc ctgctgagat 300
 ttttaattggt attttgcttg ttctgcagct taatgcaaga aaattatctt aacaatattg 360
 aatttttcaa tctattaaca tggtatatat tactgtttac ttaggatttt ttcacttttc 420
 ctgccttggt ttgaactgat attgtggttt taagtaattt tttttatttc tactattggc 480
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 ttgaattgtg catgtccaat tgtctatgg 569

<210> 204
 <211> 266
 <212> DNA
 <213> Homo sapiens

<400> 204
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 tgaggctgca gatgagactt gtccccagct ggctgtccat cctcctgggtg tcagcaagct 180
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 ccctgtggta actttgcagg cggccc 266

<210> 205
 <211> 506
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (41)..(41)
 <223> n is a, c, g, t or u

<220>
 <221> misc_feature
 <222> (99)..(99)
 <223> n is a, c, g, t or u

5

<220>
 <221> misc_feature
 <222> (103)..(103)
 <223> n is a, c, g, t or u

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 45 gctgttgagg gcctctgttt cccctgtgct gggggccttg agtgctatgc tagcangggc 480
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 <213> Homo sapiens
 <400> 228
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 ttgctcactg gctgctggct ggggctgtga agctgtccag tctagaactc aaagagtgat 120
 5 ggtacaggct ttagagcc 138

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 10 <213> Homo sapiens

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 15 <223> n is a, c, g, t or u

<400> 229
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 20 gaggagtgcc agctccatat gcggtctccc ccatcagtca ggccagcagc gggttcagct 180
 gcctctgggc agccctancc catacagaca gggagacctc cctcccgatc ttctgtgaat 240
 agtcccttat acccctgctt atgcctcagg ggctcctcca cccttttgtc ttcatactgc 300
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 tgtgcacatg tgggtatgtt ctcagccatg tgtata 396

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 30 <213> Homo sapiens

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 35 <223> n is a, c, g, t or u

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 aaagctgttg aaaaatagga aaacaaaggg cattgttcac agatagggcc aagtctcccc 180
 45 ttgcaagggt gcctctgttc tgtccctgcc cccacctcac cttctctact cctccagtaa 240
 gttggcagtt ttgggtgccaa accccaaatc tccaaagaga catgccaggc aagacaaacc 300
 cccaaacacc tcctttccgg tggccttgga aacagattgc tccgagctgg agaatgtcgg 360
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 ctgcctggag gg 432

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<211> 549
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 <213> Homo sapiens

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 accaagcgga gttgggcttg ggaaggcaag aaggtgccag aggccctgga gatgaagaag 180
 10 aaaacaccag cagccccage aaagaaaacc agcactacct tcaacatcgt ggggaccacc 240
 tatcccatca acctggccaa ggacactgaa ttttccacca tctccaaggg cgctgctccc 300
 agtgcctcct caaccccaac aatcattgct tcacccaagg ccacctacgt gcaggacagc 360
 15 ccgactgaga ccaagaccta caacagtgtc agcaagggtg acaaaatttc ccgcatcatc 420
 tttcctgtgc tctttgccat attcaatctg gtctattggg ccacatatgt caaccgggag 480
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 20 tgtataccc 549

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 <212> DNA
 <213> Homo sapiens

25 <400> 232
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 30 gtggaaatga aagaaaccct gactttccca ctaggaagga agagactgtt ccttcttgtg 120
 atgtactctg aagaaaaatt ctaggatttg gacagatttc ttgggttata aaacatgatt 180
 tttctctctg tttcttgggc ttttataatg ggtactgttg ttttcttgca aagctttaat 240
 35 gattccataa ggacttgat aaagtttatg ggagaatttt caatgtagat gtgaatggca 300
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 ggagacacag atctaaattt taaaggtggt ttgggccttc tcaatcatat attaaggtcc 420
 40 ttttatgtta tagataagta aattaaggcc cagaaagatt aatagcccaa ggtcccaaga 480
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 tatcaaaacc aacc 554

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 agtttgtaat gaattcaagc tgagttctct cgaggggaaa acatgtataa ctacagttcc 180
 55

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 5 agcaactgga aatatatttc gtaatttcat tttatgtgtg attttaaaag ttaagctact 360
 tcaaaaactca tctgtctaac ttattttcac taataagtgt aacttgccctg gaatttggca 420
 gatctaagct gggcttgggc tagatggttt caagcctgag tcattaagat gtgaaattta 480
 10 cagaaacaac agaggattga ggaacaagtt aaaggacact ctaatgggtgc agtctgcat 539

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 15 <213> Homo sapiens

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 25 catcagcact gttgcctttg aggctggcct gcttgaatgc acacctgagc tccggattca 180
 cagtggagga agccagatgc catgtcatga ggggtgctcaa gcaacttttt ggagatgtat 240
 gtatggagag aaactgaggc ctccctgcaa cagccagcac taacttggca agcatgtttg 300
 30 agagccacct ggggaagtga gccttcagcc ccagttaagc cttcagatga gactgcagtc 360
 ctggccacca tctggactgc aacttcacaa gagctcctaa gccagagcca tgcagatgga 420
 ttcttggccc c 431
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 <210> 235
 <211> 403
 <212> DNA
 <213> Homo sapiens
 40
 <220>
 <221> misc_feature
 <222> (139)..(139)
 <223> n is a, c, g, t or u
 45
 <400> 235
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 acagaagttt ccaggctctt cttcacctga actgtgtcta aagcaagttc cctccacctt 120
 ctgtatttat acgcttgant ttttaaaacc taaatgttgg gcttcacatt tgttccttgt 180
 50 aaatttcata ttgggtgatt cagtctaccc tctggccttt aaaaattgtc tgagccttga 240
 ttcgatcatg aaaccagctt acccttcccc tgtgtgctgg cccagtttt ctaaccaggt 300

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gttcaactgt gccctttggg gctgtggttc atttggctct gat 403

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<211> 257
<212> DNA
<213> Homo sapiens

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gactgtcacc atgtcactac ggcactctcc agctgctgac caaagccctc gctaaccgca 180
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gccctgccat actctgggtc tttcctctgg agcaaggtag agagactgca gcgaggcgtg 240
gaattgggaa gctcttc 257

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<210> 237
<211> 446
<212> DNA
<213> Homo sapiens

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ccgaggcccg gcggcgctgc gaccgcgaca gccgctgcaa cctggcgctg agccgctacc 180
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tgacctactg cggcaaagtc ttcaacgggc tgcgctgcac ggacgaatgc cgcaccgtca 240
ttgaggacat gctggctatg cccaaggcgg cgctgctcaa cgactgcgtg tgcgacggcc 300
tcgagcggcc catctgcgag tcggtcaagg agaacatggc ccgcctgtgc ttcggcgccg 360
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aggactacga tgacgagcag cgcacc 446

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<211> 340
<212> DNA
<213> Homo sapiens

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<400> 238
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ggaagcccg ggcacctgga ggggactggc tgaccttctt cattcttttc aagtgtgaat 120
aataaccaag ccagtttg caactccttg aggggtgagga cgaagcccca ttctcctttt 180
tggaacttgg tggggctcag gaagcaggtt ctctccagtc ggtggctttc ctttctgttg 240
50
cgggtctctt gagggcctgc cttcatgaag gcacatgagt gactcatcat ttgtgaatta 300
attgctatat gtgaagggca tctgagaaca aattatcttc 340

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<212> DNA
<213> Homo sapiens

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<400> 239
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tgctatcacc ttccagctgc ccatgtgcac taacaagttt attgatcaca tatcctgtga 180
actcctagct gtggctcaggc tggcttgtgt ggacacctcc tccaatgagg ctgccatcat 240
gggtgtctagc attgttcttc tgatgacacc tttctgcttg gttctgttgt cctacatccg 300
gatcatctcc accatcctaa agatccagtc cagagaagga agaaagaaag ccttccacac 360
gtgtgcctct cacctcacgg tggttgccct gtgctacggc acaacgattt tcaacttacat 420
ccagcccccac tctggtcctt cagtccttca agagaagctg atctctgtct tctatgccat 480
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ctggcataaa ctattagaga 560

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<211> 524
<212> DNA
<213> Homo sapiens

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ggtaagaaaa taaaaatcaa taatatcaac attatgaata ttttaggtac ttaggaattt 180
ggggtagaat gatggaaagc aaactgttaa ttatagctgt atatttcagt gtagaggcta 240
cagggtgcctt gcatttgttt tcttataaaa tctgttccca tacattttac ttactttatt 300
tgaatttagg aaactttcat taggtagcca tttttatttt ctgtttcttt aatcatttta 360
ctttgaaata attttaaatt tacagaaaat ttgcaaaaat agtgtagaaa tttcccat 420
gcctttatcc agcttctgt agtggtgcca ttttatgtaa ccatagtaca attattgaaa 480
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<212> DNA
<213> Homo sapiens

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<223> n is a, c, g, t or u

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 <221> misc_feature
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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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<220>
 <221> misc_feature
 <222> (346)..(346)
 <223> n is a, c, g, t or u

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 <222> (390)..(390)
 <223> n is a, c, g, t or u

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<220>
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 <222> (474)..(474)
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 agatcacaag tagaaccttg atctgaaaca tggcatgtgg cgatttatat tgagtattag 180
 gttaaaaatg caagaangga gcatagttaa tattttacnt taaagctaaa acnataattg 240
 cctacttaaa attttcagtt aattagggtg tcactttttg ttcttaacna agaaatcaac 300
 tagttttant ccataaacag ttagaactga tgcacacatc cgtttntcct tactcatttt 360
 aacagctat ctgaaatagg aagtgtaatn taatntttta agaacttgaa aacatgacag 420
 aatgtttta actataaaca tatattgtat atggttagcat attgtatata ttgnatatta 480
 acataagcta gaatcattga cata 504

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 <211> 317
 <212> DNA
 <213> Homo sapiens

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 10 acacaacgat gacgcactac tcaagaacta cgggctgctc tactgcttca ggaaggacat 180
 ggacaaggtc gagacattcc tgcgcacgt gcagtgccgc tctgtggagg gcagctgtgg 240
 cttctagctg cccgggtggc atccctgtga cccctcccca gtgcctctcc tggccttgga 300
 15 agttgccact ccagtgc 317

<210> 243
 <211> 437
 <212> DNA
 <213> Homo sapiens

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 tgtggggggc agaacacagt gcccggagtc aggaactacg gattttggga taaagataaa 120
 25 agcagatatg atgttttctg ttttacatcc aatttcaatg gccgttttta ctatctgac 180
 caccaccacca aactgacctg tgatgaagcg gtgcaagctt gtctcaatga tgggtgctcag 240
 attgcaaaag tgggccagat atttgcctgc tggaaaattc tcggatatga ccgctgtgat 300
 30 gcgggctggt tggcggatgg cagcgtccgc taccctctct ctaggccaag aaggcgtgc 360
 agtcctactg aggtgcagc gcgcttcgtg gggtttccag ataaaaagca taagctgtat 420
 ggtgtctact gcttcag 437

<210> 244
 <211> 389
 <212> DNA
 <213> Homo sapiens

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 <222> (299)..(299)
 <223> n is a, c, g, t or u
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 <400> 244
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 atttttacaa tgctatttat taacaatata tgacaagagt actagaaatg ttacttgtga 120
 50 ctatcttgct tattctagcc aagctggatg cctggctgtt tctcagttat actaaatgag 180
 ttctgctctc agggctcttca tacttgccct tccctctgcc tgcaacactc ttctccagt 240
 tttttttttt tttttttggc tctctccatc actttaggct tccattaaaa ctgtcagc 300

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tcagggaagt tgccttcctt gaccacaacc acactaattc aaataccaat ccttccccgc 360
ctccgttttg taactctcta gtctcttat 389

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<211> 136
<212> DNA
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<223> n is a, c, g, t or u

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agaggccnnt tgtttgctcc gagtgctaaa naaggcttct tccagatata agacctacgg 120
gtgcatcaga taattc 136

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<211> 369
<212> DNA
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ggctgcagggt gtcctcaga ccttagggaa acatttgagg gggagcttgt tgaggagata 180
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cttttcctt 369

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<212> DNA
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tactaacaaa gtggctgcag gagatttttg aacggctggg ttaaattggc tcaggagact 180
tcagtttttt gtttagctac atgattgaat gcataataaa tgctttgtgc ttctgactat 240

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 5 cagtcataga tgggtgtgaca gtgttttaaac gcaacaaaag gctacatttc catggggcca 420
 gcactgtcat gacccctcact aagc 444

 <210> 248
 10 <211> 394
 <212> DNA
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 gaggatccgg ggcagctcct gaccctccac agccacctgg tcagccacca gctggggcaa 240
 20 cgaggggtgga ggtccactg agcctctcgc ctgccccgc cactcgtctg gtgcttgttg 300
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 ccttgtcatg gaccatgggc gtgaggaagg gctc 394

 25 <210> 249
 <211> 414
 <212> DNA
 <213> Homo sapiens

 30 <400> 249
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 actcttgaga agtaatTTTT attttcagaa ccattttaca gatttaaaat aaacagggttt 120
 35 gaggaattag ttttaacttat ccaaagtttc gtggctatta agttctagta tttggagtca 180
 aatgcaagtc tgtctaaatc tagagcccat gttctttaac tgcaacacta taatgtctca 240
 ccccgctcta gtcccaccaa ttagtcaact cttttagggc agaagtctgt ctaattcatc 300
 40 tttgcttcct gttactttat atttaattaa aaattttagt gactttttaa cttgtaaatt 360
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 45 <210> 250
 <211> 268
 <212> DNA
 <213> Homo sapiens

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 ttttacaatt ttaaactcaa atatgattta gtattatgca cataatacaa acagtagtgg 120
 tgagcaaacg tgtgtttccc ccacatgtgc agaatatgat ggattttatg aaaataaata 180

 55

ttcttaactc caggaaatat gatctatatg gttccttaaa agattttcca atacactgaa 240
aatttagttc cttatgttca ttgtataa 268

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<210> 251
<211> 443
<212> DNA
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<223> n is a, c, g, t or u

15

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<223> n is a, c, g, t or u

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aagcatccag caactgagta atgcttccat tggggaactg gagcaggtgg tcggacaagc 120
agtggcacag nnagatccat gccttcttca cgcagnccca ggtgagggct ggcctcaggg 180
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aagagaatgg gccgggtgca ctggctcacg cctctaattct cagcactttg ggaggccgaa 300
gacagcggat catctgaggt caggagtcca agaccagcct ggccaacatg gagaaacccc 360
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aggccgaggc atgagaatca ctt 443

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<210> 252
<211> 281
<212> DNA
<213> Homo sapiens

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aactgttaaa ggaagccctt cctcatctac agattaattg ctcccatttc accaccattg 120
ccaggccaac tattggcaac aaaaagaacc aggagatatg gggcatcaaa tgccgactga 180
cactgcaaaa gccagttgt ctatgaagta tttattgcag gatggtgtct cttctttaga 240
acagggaaaa taggcaggaa gcccaattgc tggagtactt a 281

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<211> 249
<212> DNA
<213> Homo sapiens
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10	gctgatagat ttcccccaga gagctattca aggacttcct aagggtgggtg gactgcaggg	180
	ttagggacacc tgctatagag gtgacatttt tccaaggaca agcagggact ttgggtcttga	240
	ctgttctct	249

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<210> 254
<211> 259
<212> DNA
<213> Homo sapiens
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	ttaagctcct	tcccgagaag	cacgagattg	aaaacctgcg	ggcattcaca	gaggagcgag		180
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45	ccagttactt	ggatggattc	ccctattgaa	gtttatacaa	atgatagtat	tttggatgcc			420
	tgggccgatt	gatgatggct	gtcctgcaca	gcctgagaag	gagggtatgt	tgatgaatgt			480
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 ctttagaaac ctgattcaac ttaaccgaac ttcaggaat ctgattccta agctgagtat 180
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<211> 532

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<222> (152)..(152)

<223> n is a, c, g, t or u

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 gctccaatat ccgttatttt ccaaaggatt tngtatcttt ttgaaaatgt ttacatcatc 180
 agatgatcca cagaattcac tttatgtgag atctcccgag agtttccatc ccaacataat 240
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<223> n is a, c, g, t or u

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	gcnagtgcac agggagtgtg tgcagccttg tgaagggtg ggaccacttg cccagactgg	420
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	gcgggagtgt ggaggagggt gggcctctca cccaggcttt ctggccccct ctccctcagct	180
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	cgggcgcaga tgaaccagat tcagtctgtg gaggtttgac attcacctgc ctgggtcac	420
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 tgggtctgcc tggagaaaa 379

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 <212> DNA

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<213> Homo sapiens

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 tttgacgctg tttctcatgg tctccgacct aataaagcaa gataagagaa aacaaatggt 180
 attttaaaaa aatcaccctt tggcaaaaga aacatgtaaa attagaatct ggcacaaaca 240
 aaacctgaat ctgggttggt aactttcacc acccgccgca actctttgat aaaacctcaa 300
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<211> 507

<212> DNA

<213> Homo sapiens

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 aaaaagctgt gttcagagtt aggagaatat atccaataaa agatgggttc gtctaccaat 180
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<210> 266

<211> 202

<212> DNA

<213> Homo sapiens

<400> 266

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 5 gaaagcctgg tggtgaaaga aa 202

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 10 <213> Homo sapiens

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 15 tcctccttca cccctgaatt tccagagcac ttcactctgct ccttcacac aagtccagtt 180
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 35 tctgaaagtc acttttctca tcagttaaata gggggcaagg gtccgtggtc cgaccaaggt 180
 cttgggttca cagacatcac caggagcctg catgccctg atcactcctt ctcccttcctc 240
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 cctgggagac agagcgagac tctgtctcga aaaaaaaaaa ggtccgtgcc aagctgctcc 180
 ctgcccttgc ctttccctt tccctggggg ccaaaccaca tgtgtcctgc ctctcctggc 240
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 5 taataaagga gg 372

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aactccttc 189

50 <210> 277
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 <212> DNA
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	cctgggtgct gtggatgcat cctgctgct ggaaattctg tgctctctgt ttccatccct	180
	ttgtcgtggt aatgaccgta tacctctccc ctgtaccctc cntgcntgc tctccgtgca	240
50	ggccctctc cctctggttg tcccatcagc atttcccccac agctcgttgt tctccttcc	300
	tcttttctgg tgaccttct actgattgca ttgtacctct ttccctgata ttaaa	355
55		

<210> 304
 <211> 362
 <212> DNA
 <213> Homo sapiens

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 10 accccggagg cacctgggga gcacggcctg gcacccatggg aacaggggag cagggcagcc 180
 cctttgcagg aggtctgtgcc acggacacaa gccacggggc tcaccaagcc taccctacct 240
 ccgagtcccc tgatggcagc cagaagacgt ctctagtgtt gcgaacactc tgtatgtttc 300
 15 gagctacctc ccacacctgt ctgtgcactt gtatgttttg taaacttggc atctgtaaaa 360
 at 362

20
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 <211> 533
 <212> DNA
 <213> Homo sapiens

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 ttcgacacca taacaacagc tactcaaact gtaaaccagg ataagaagtt gatgacttca 180
 cactgtggac agttttttcca aagatgtcag aacaagactc cccatcatga taaggctccc 240
 30 acccctctta actgtccttg ctcatgcctg cctctttcac ttggcaggat aatgcagtca 300
 ttagaatttc acatgtagta gcttctgagg gtaacaacag agtgtcagat atgtcatctc 360
 aacctcaaac ttttacgtaa catctcaggg gaaatgtggc tctctccatc ttgcatacag 420
 35 ggctcccaat agaaatgaac acagagatat tgctgtgtg tttgcagaga agatgggttc 480
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<223> n is a, c, g, t or u

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    cgttaacatc nacacaggcc ttcagtctga tgagaaacat ttaccatcta ttgtctcgga      180
10   agcctgctac ntggaggctt catcntgatg ataaagcctt ggtctccaca accccgtata      240
    acccagacat tcctttctat tgataactct tgcaagcgat tgccaaccag aagatgttta      300
    aatccaccta taacctggaa gccccagtt ccagctgccc acctttctgg actaaaccaa      360
15   tgtatatctt caatatatctt gattgatgtc tcatgtctcc ctaaaatggg taccatcaag      420
    ctgtgcactg acca                                     434

20   <210> 307
    <211> 157
    <212> DNA
    <213> Homo sapiens

    <400> 307
25   cctccgcaca ctggatgaga atccatcttc cattcgagct gggaatagac tttgtgaaag      60
    atattatgta atggagtctc gggaaccctg agacctctcc agcgaagctg aagtgaatta      120
    attaagtgtc ttaaacggtc ttggtgctgt gttacgg                                     157

30   <210> 308
    <211> 367
    <212> DNA
    <213> Homo sapiens

35   <220>
    <221> misc_feature
    <222> (35)..(35)
    <223> n is a, c, g, t or u

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    <221> misc_feature
    <222> (38)..(40)
    <223> n is a, c, g, t or u

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    <223> n is a, c, g, t or u

    <220>
    <221> misc_feature
55   <222> (58)..(58)

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 <223> n is a, c, g, t or u
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	cnnntcnntg ncntntgcna antnnngann nanaaccgtg taaaaccatt tttatgtggc	120
	ttcaacgtca actataaatt agcttggtta tcttctagga gaaatgctat ttatcttgga	180
5	gtagtagtaa aaagggtca aaggataagg aggccattca ggcctattct gaatccctga	240
	tgacatcagc tcccaagggc tctgtgctgc aggaagcaaa actgtaggng ggtaccaggt	300
	aatgccgtgc gcctccccgc cccctcccat atcaagtaga atgctggcgg cttacagact	360
10	gaagatg	367
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	<211> 484	
	<212> DNA	
15	<213> Homo sapiens	
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	gcgtgaagaa gtgtccccgt aattatgtgg tgacagatca cggctcgtgc gtccgagcct	120
20	gtggggccga cagctatgag atggaggaag acggcgctcg caagtgtgaa aagtgcgaag	180
	ggccttgccg caaagtgtgt aacggaatag gtattgggtga atttaaagac tcaactctcca	240
	taaatgctac gaatattaaa cacttcaaaa actgcacctc catcagtggc gatctccaca	300
25	tcctgccggt ggcatttagg ggtgactcct tcacacatac tccccctctg gatccacagg	360
	aactggatat tctgaaaacc gtaaaggaaa tcacagggtt gagctgaatt atcacatgaa	420
	tataaatggg aaatcagtgt tttagagaga gaactttctg acatatttcc tgttcccttg	480
30	gaat	484
	<210> 310	
	<211> 526	
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35	<213> Homo sapiens	
	<400> 310	
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	gccaagggtg aggagcttcc cactccagga ctgttgatga aaggacaga ttgaggagga	120
40	agtgggctct gaggtgcag ggctggaagt ccttgcccac tccccactct cctgccccaa	180
	tctatctagt acttcccagg caaataggcc cctttgaggc tcctgagtgc cctcagatgg	240
	tcaaaacca gttttccctc tgggagccta aaccaggctg catcggaggc caggacccgg	300
45	atcattcact gtgataccct gccctccaga ggggtgcgtc agagacacgg gcaagcatgc	360
	ctcttccctt ccctggagag aaagtgtgtg atttctctcc cacctcctc cccccaccag	420
	acctttgctg ggccctaaag tcttgcccat ggggacgcc tcagtctagg gatctggcca	480
50	cagactccct cctgtgaacc aacacagaca cccaagcaga gcaatc	526

<210> 311
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 <212> DNA
 <213> Homo sapiens

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 <223> n is a, c, g, t or u

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 ggatgccaac aaaaacaaga taaagcttgg aatttgtaag gctgctactg aagaggagaa 120
 cagccatggc caggcaaattg gtcttctcaa tgctccaagc cttgggtcac caattcgtgt 180
 ccgctcagag attactcagc cagacagaga tattccactg gtgcgaaagt tacgttccat 240
 tcacagcttt gagctggaaa aacntctgac cctggagcca aagccagaca ctgacaagtt 300
 ccttgagacc tggtataaa 319

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<210> 312
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 <213> Homo sapiens

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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 <222> (92)..(92)
 <223> n is a, c, g, t or u

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 <222> (97)..(97)
 <223> n is a, c, g, t or u

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 <222> (186)..(186)
 <223> n is a, c, g, t or u

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55

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5
 10
 15
 20
 25
 30
 35
 40
 45
 50
 55

gggggtagat tgcagttaca aaatnnncnn cngnngngtg ttcggcgcgg ttccccagc 120
 tgtctctggc tgaaccggcg ctctcgctc cctgccgaac acagcgtgag gagccccccc 180
 aggganatgg tgtttgagtc tctgggcttg ccgagcacta agtcctctga gttc 234

 <210> 313
 <211> 125
 <212> DNA
 <213> Homo sapiens

 <400> 313
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 gtccatgctc cacttctctc caagggtgtc atggccattc aactcaacaa tcaaaccaaa 120
 gccaa 125

 <210> 314
 <211> 446
 <212> DNA
 <213> Homo sapiens

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 <222> (53)..(53)
 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

 <220>
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 <222> (211)..(211)
 <223> n is a, c, g, t or u

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 cttttttaan catttcttct cttctttctc ttttttatca ctaaatgaat gacatgtgga 180
 gaaactattc agctttttaa gtatnctcca nttacttgtc tcaactacca ctattttattg 240
 tgtttatcaa aatcataaaa agtcattttt tggcatttac cttcgtggtt gagactgctg 300
 tctgtatgtc tgggaatgga agtcctcttc agggattcag caagggtgt acttttgctt 360

aatactagtg gttccttatt ctaagtgatg acatcatcca cctttcctag aaatgggtct 420
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<210> 315
 <211> 473
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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 aggagctggg ccatcctgtg gtggatcgat caattaagat tgccatgact acttgtgagc 120
 aaatagtcag gaaggatttt gccctggatt cggaggaatc tcgaatgcga atagcagctc 180
 atcacatgat gcgtaacttg acagctngga atggctatga ttacatgcag ggaacctttg 240
 ctcatgagca tatctaccaa cttnaaaaaa cagttttgcc tcagcccttc gtgtaagttg 300
 gctatttcct tggatatagg acaaaacgta ttactgcttg tctgtaataa tttttttctt 360
 tgtctatata tggcncctgg cgttaccact tattnttaat aatcnccata tttgtttgat 420
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<210> 316
 <211> 576
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 <222> (351)..(352)
 <223> n is a, c, g, t or u

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 <221> misc_feature
 <222> (395)..(395)
 <223> n is a, c, g, t or u

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 caccctcaaat cacatctctg ccctcaaaca tcgcgctgtc ccctaccttg ccgcagtcctc 180
 tggccccctc ctaggaaggc ccgggtccca caggcaacac ctaagtggac caaccctctc 240
 gcctgtcctg cccccagac gatgactgaa ggctcctttg acaccttgag atgattctgc 300
 tactttccag acttttctta caaagcaaac acttttattt tctatgcaaa nntgattcag 360
 agaatttata taaaggcggg cgaggggcag ccgancaggg agctttggga cagggctggg 420
 gcccccatat ccccccggg ccacctgctt tccctcctat ggctcccctg gaacaggagg 480
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 cgggcctgag ctccagcatc tgagtttggg ggtatg 576

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<210> 317
 <211> 265
 <212> DNA
 <213> Homo sapiens

35

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 gcctgccgag acccggcaga aatccaggag ggacagatca acatcgccat ggcctcggcc 120
 tcgagccctg cctcttcggg gggcagtggg aagttgcctt ccaggaaggg ccgcagcaag 180
 aggggcaagt gaccttcaga gcaacagaca tccctgagac tggtctccct gacactgtga 240
 gagtgtgctg ggaccttcag ctaaa 265

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<210> 318
 <211> 515
 <212> DNA
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 gaccagaata tcacaaatgg gtgatgtata atgtctcttt agtttttngg tattnggcct 120
 20 ctttttaaagc ctgtcggatg tatgggagaa aacaatgaac gtgctttgat ttcctatcag 180
 tcaactcttaa gaacatacat atngtttaag taactcggtc ttttttatct gattcttgag 240
 ncactatggg tagcaagtaa ccacttaca atttaaagt aatatacact ctttttctgt 300
 25 gtgtcaagtc cttattttta ggtgcatatt gacattttaa tgtaattat tgtttggeat 360
 ataatatcaa aaatctatta tttattttat gctgttacag ttaaagatg tgatttatga 420
 catactgaat caacttgcct tccaatttag tgtgtaatat ggtaagcatt tatactttta 480
 30 gatatgtctt atttttatgt ggatgcctgt ctacc 515
 <210> 319
 <211> 541
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 35 <213> Homo sapiens
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 <223> n is a, c, g, t or u
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 <222> (167)..(167)
 <223> n is a, c, g, t or u
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 <222> (172)..(172)
 <223> n is a, c, g, t or u
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 <221> misc_feature
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 <223> n is a, c, g, t or u
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 <223> n is a, c, g, t or u
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 <221> misc_feature
 <222> (260)..(260)
 <223> n is a, c, g, t or u
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 <222> (509)..(509)
 <223> n is a, c, g, t or u
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 agggatattg gagaanatat nccactngac aaagatttnc ngaaatngaa anattattca 180
 ntcattcngc naatntagga taagaatgat aattgctgtn acatcttata aacgatatct 240
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 ttgggctaca gttacaattn cagaggcatt ggcgtgctta tttagaaga aaacaagatc 300
 aacaagata tgaaatgcta aaatcatcaa ctcttataat ccaatctatg ttcagaaaaat 360
 ggaagcaacg taaaatgcaa tcacaagtaa aagctacagt aatattgcaa agagctttta 420
 55

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gagaatggca ttttaagaaaa caagctaaag aagaaaattc tgctattatc atacaatcat 480
 ggtatagaat gcataaagaa ttacggaant atatttatat tagatcttgt gttgttatca 540
 5 t 541

<210> 320
 <211> 495
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 10 <213> Homo sapiens

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 15 <223> n is a, c, g, t or u

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 20 tttttttcag tctttttttt ttttnnagaga gggctctcttg tcaacgcaag actgggagtg 180
 gcagtggcac gatcttagct cactacaact tctggcctcc caggctcaag caattctcct 240
 gcctcagcct cctgagtagc tggggattac aggcattgcac caccacgccc agctaatttt 300
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 acctcaggtg atccaccac ctcggcctcc caaagtgtg ggattatagg tgcgagccat 420
 tgcgcccagc ctcagttatt ttatttaaca gtgtaagtac ttagaaagta agaaaatggc 480
 30 gtgattagtt ttttg 495

<210> 321
 <211> 429
 <212> DNA
 35 <213> Homo sapiens

<400> 321
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 tcagatctct gagaacttgt ttagcaacaa agtcctcaat gccttgaaac cagaaaaaga 180
 tgtggatgga gtaacagaca taaacctggg gaagctggtg cgaggggatg cccatgaatg 240
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 cctagatgga aagaagattt tggtagtggg ggcccatggg tctttggaag ctgctctaca 360
 atgcctgttc cagagaaaag ggtccatgac aatgagcatc cagtggaaaa cacgccagct 420
 50 tcaaagcaa 429

<210> 322
 <211> 467
 <212> DNA
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<213> Homo sapiens

<400> 322

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 aaccccttgc tacagatgcg ctggtttctc cggaagacag ggcactatca cagtttccact 180
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 ggagtagcga tgtatgctgt gtcttgggtgt ttcattgttta gcatctggcg ctttgcattg 360
 aggaagagca tcaagaagta ccatgcttgg agaagcaggc ggagtgagga acggcagctg 420
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    agatttcttc tcttttagtat aattgacctt ctttggtagt ggaatagtga atacttacta      180
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    aatgtaactt attatttttt ttgagaccga gtcttgctct gttaccagg ctggagtgc a      360
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<212> DNA

<213> Homo sapiens

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<211> 239
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ggaccttttg ca 432

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gata 544

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<212> DNA
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cagtgtccag cctgctgaag gtgttcaacg accagagtgc ctcggaccac atcgtgcagt 180

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 5 tgaaaaaatt gagaaaattg aactcagaga tcccgatccc aaccctttc tcttgggagt 480
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 ttggtaaagg tttaaagggg actttgttcc accagggagc attttatttg ggcgtctcac 420
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 50 atggatgccg aggagtctga acctaaagac gtattgcccc atggggatgg gacctaccag 240
 ggctggataa ccttggctgt acccctggg gaagagcaga gatatactg ccagggtggag 300
 caccagggc tggatcagcc cctcattgtg atctggggta tgtgactgat gagagccagg 360
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<211> 186
<212> DNA
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ccaaaa 186

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<212> DNA
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tggctgcttt tgcattagga tgacagaggt gaatagttgc aacagagact ggctgggtctg 180
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 aatggatggt tgaattaact tcagcatcca agtttatgaa tcgtagttaa cgtatattgc 240
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20 agcctctttc tgtgagatta ataaatgaat aaatgcctcc atatttttca a 291

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<212> DNA
<213> Homo sapiens

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gccagagaat gtcttcagg agttctgcta cagagaagag agtaaccccc atccatcatg 180
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40 ggggttctgc aagcaactg gatgacgacc gaagaaacct tgcgcttct gagaagacac 300
ccaatccaag aat 313

<210> 363
45 <211> 318
<212> DNA
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gttcaagaaa ttctcatgtc tcagcctcct gagcagctag gattacagac aaaccttgga 180
aatcaagaaa gttctggaat gatgaagctg ttcatgccaa gaccgaaagt gctggcccag 240
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45 caaaacatac aataaacttg tgtaatttt tctatcaaag tcagaattta ttcataagga 360
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tgcacaatct gattgggcat gtcacctcgg atggcaaggg agtggaagtg gtcaaaatca      180
30 tggagtccca gctttcggga                                     199

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gaaattttaag tagaaattgc taaccgaaga ctttgctaag caaaccagg tctgcttgat      240
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 aatcttatta ctactaggag ggtaagaga caaaactatt aaaaacaact gcagctacag 240
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<213> Homo sapiens

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<211> 289

<212> DNA

<213> Homo sapiens

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gattgaagcg tactctgtgc ctactagatc ttttcacagc caaaaacacc tggcaaccct 180

tggagaagta actattcctt tttttcacia gtaagaaaat agagcctcag aaaattttaac 240

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agnaccctgt ggactcaacc ctctggttga acaacataca agataatatg agacatttat 180

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cacttgctcc tgttgattct ggaaaggagc aacggcatct tatgaagctg tagcagatac 300


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cctgatattt atttcacaaa aaaactgaaa ttgctttgtg tgtccaggct tgaatgttta      180
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aggcatactt gattaatata tgtgtgctga gtgcttctctg                                         220

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cacnggacta tnagttactt gaaagctgag gcttggtaga gggctggagc caattgcggt      180
aaactaacta acattattgc aaaatatatt ctagggtttt tactctaata aaaatgactc      240
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 aatatcttct ggctgaacaa gggcggttat gcacagtaat aaaccacatc tgttggttctt 420
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<212> DNA

<213> Homo sapiens

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ggatatacag agagccaaag gcccatggga cgtgaccaac attccactga gtctatacga 180
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<213> Homo sapiens

<400> 402

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cataatgatg cttcttcctg ttaaatttac aatgaaggga aaccatcac ttaactgtag 180
gaatttccca aaatgaactg atgaccagtg atctctctat cagaaaatgg cagatttcta 240
gccttccaga actttgattt tcttgacat tcaatgggtc ctttttccca aatatttttc 300
aactgatgcc aaaccttgga tttggtttaa tccaccttg gtttaggttt ggggaccctt 360
ttcttgacc gtcccagttt tgggttaaac cgatttgat gaccctgtga gtcgccactg 420

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<211> 512
<212> DNA
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agttgctttc attcttcctc aaagtattta ccatcagcta cagtccaaaa ttgctttttg 180
15 ttcgaaggaga tttatgaaaa gactctgaca aggactcttg aatacaagtt cctgataact 240
tcaagatcat accactggac taagaacttt caaaatttta atgaacaggc tgatacttca 300
tgaaattcaa gacaaagaaa aaaacccaat tttattggac taaatagtca aaacaatggt 360
20 ttcataattt tctatttgaa aatgtgctga ttctttgaat gttttattct ccagatttat 420
gcactttttt tcttcagcaa ttggtaaaagt atacttttgt aaacaaaaat tgaaacattt 480
gcttttgctc cctaagtgcc ccagaattgg ga 512

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<211> 229
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35 ccttactttg aaacaccact ggctcccttt cccaatggta gttttgtgaa tggctttaat 180
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<211> 495
<212> DNA
<213> Homo sapiens

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cctgggctcc ctctgctact cccaggaaat gggctcctga cacagcagtc tgccaccaca 180
gccccaggag ggtgtcaaca ccagcaaata ctgtatttgc agcatgtcca agatgaccct 240
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ctctaggcat ggtgaacgcc tgggaccaag ccattgtggc ttttttattt tgcctttctg 360
gaagactcaa gatatgtctc ttcattctct ctcagtattt gtttactttg gtttttttgt 420

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ttttaatctc agagagaggt gtgttttagtg ggcacaagct gtaatatcca gcaaaaacttt 480
gtcgactggc actgt 495

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<212> DNA
<213> Homo sapiens

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<223> n is a, c, g, t or u

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<223> n is a, c, g, t or u

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ccagcagtgc cctgccctgc agtctgagct accagattcc ttgtgaagat aatttgagga 180
ccatgactca cccaaccaca tttcctgggg cctcaaattg aaaattcagg atgggctttt 240
ctatatgact ggctgatatc caactatgcc atggctctta catgccatga acattctttc 300
ctgccagagt tctaagaatc tgtgttctct gccttagacc ttctgcagat gagccacag 360
gaagctccac gtgtagctga gctacatgca ccaggcctca gtttgcccca agtcccctgt 420
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ggttcaatga acatttgaaa gaaaacaagg ttgcagaccc tgtggattct tctaacttgg 300
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<210> 408
<211> 397
<212> DNA

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<213> Homo sapiens

<400> 408

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 aattctatct ccactgtgaa gcattatcat ggtgtggcca tatatgatct atccctatct 240
 gaagtcactg cattttattcc ctgacccctca tttgcaggtc cagtaccttg tacaagtttc 300
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<210> 409

<211> 48

<212> DNA

<213> Homo sapiens

<400> 409

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<210> 410

<211> 459

<212> DNA

<213> Homo sapiens

<400> 410

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 caaccgacta gaggacctgg gtcccggcag ctctttgctc acccatctcc ccagtcagac 300
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<210> 411

<211> 275

<212> DNA

<213> Homo sapiens

<400> 411

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 catagacaga ccaagaaatg gcggtggagg gcatctggta gatgacacgc gcctggatgc 180
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ccgacagccg gccgctgatg ttggccagcg agagg 275

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 <212> DNA
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<400> 412
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 tccttacttg tgggatcaaa tgctgtaatg gtggaggtgt gggcagagga gggaggcaag 240
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 <223> n is a, c, g, t or u

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 nccccacatg cacacacttt taaaatctat ttttattctc ttgctaaagt tgtaattatg 180
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<210> 414
 <211> 166
 <212> DNA
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<222> (27)..(27)
 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 attggtggca ttcncaaagc taataggac gtttatatca agaaacattt ctgtatatat 120
 tgttgaattt tagttgtaca tatactttgt atgtttttgt cttctt 166

<210> 415
 <211> 552
 <212> DNA
 <213> Homo sapiens

<400> 415
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 ggtgctccag ggggtgaagca ggccagaatc ctgggggagc tgctcctggt ttgagctgca 180
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 gagaaggggtg tctgccccca acctccctg tgggtgtcac tggccagatg tcatgagggg 360
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 cgtgtgccat gttgcacttc tgcccaggca gcagggtggg tgggtaccat gggtgccac 480
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 acataaaaagc at 552

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 <211> 524
 <212> DNA
 <213> Homo sapiens

<400> 416
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 cacaccaagc tcatcttgtg ccactgatg gcagccgtga cctacatcga cgagaagcgg 180
 gacttccgca cataccgcct gagtctcctg gaggagtacg gctgctgcaa ggagctggcc 240
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 <211> 378
 <212> DNA
 <213> Homo sapiens

<400> 417
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 ctttgttttc tgagaagagg tttgaagaca ttttattaac agcttaattt ttctctttta 180
 ctccatagga acttatttta atagtaacat taacaacaag aatactaaga ctgtttggga 240
 attttaaaaa gctactagtg agaaaccaa tgatagggtg tagagcctga tgactccaaa 300
 caaagccatc acccgcatc ttcttccttc ttctggtgct acagctccaa gggcccttca 360
 ccttcatgtc tgaaatgg 378

<210> 418
 <211> 116
 <212> DNA
 <213> Homo sapiens

<400> 418
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<210> 419
 <211> 147
 <212> DNA
 <213> Homo sapiens

<400> 419
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 aaaataatgg gtgaggcagc tagttag 147

<210> 420
 <211> 310
 <212> DNA
 <213> Homo sapiens

<400> 420
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 atcaaattctt gctttttttg aagtcaaagc tttattttca ttcagctttc ttccaccact 240
 ttctgtggta ttcttagcac cacctttcca tgtatctgga gtgataacag taccaagttt 300

cttttcacat

310

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 <211> 154
 <212> DNA
 <213> Homo sapiens

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 <223> n is a, c, g, t or u

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 cacaatgaaa caagcaatga aagaactaca gtta 154

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 <211> 444
 <212> DNA
 <213> Homo sapiens

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 <221> misc_feature
 <222> (92)..(92)
 <223> n is a, c, g, t or u

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 <220>
 <221> misc_feature
 <222> (264)..(264)
 <223> n is a, c, g, t or u

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 <400> 422
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 aacaagaaag tgaccacacc aaagcctccc tnggctgggtg tacagggatc aggtccacag 120
 tgggtgcagat tcaaccacca cccagggagt gcttgacagac tctgcataga tgttgctgca 180
 tgcgtcccat gtgcctgtca gaatggcagt gtttaattct cttgaaagaa agttatttgc 240
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 tcactatccc cagcctcaag gagnccaagg aagagtcatt cacatggaag gtccgggact 300
 ggtcagccac tctgactttt ctaccacatt aaattctcca ttacatctca ctattggtaa 360
 tggcttaagt gtaaagagcc atgatgtgta tattaagcta tgtgccacat atttattttt 420
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 <210> 423
 <211> 510
 <212> DNA
 <213> Homo sapiens

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<221> misc_feature
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 <223> n is a, c, g, t or u

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 <221> misc_feature
 <222> (454)..(454)
 <223> n is a, c, g, t or u

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 <222> (462)..(462)
 <223> n is a, c, g, t or u

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 gcaaggagcc caggcccccct cctgcctcc tccttctctgc ctgtgatgct ccgtctcaaa 420
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 cagccgaaac ctgtcttgca atggggggag gggngcggtt ctttttctt cttcttggt 480
 tcctcttatt cttccacaaa ccattctcaa 510

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 <210> 424
 <211> 191
 <212> DNA
 <213> Homo sapiens

<400> 424
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 gtcgagagct gacagaaagg tttgaagatg tttgggtggg atctgggcct ttgaccttac 120
 ctcagactag aggcgatgga aagaaaatag ttagttacca ggtgattggc gaggacaacg 180
 40
 tggcagtcac c 191

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 <210> 425
 <211> 186
 <212> DNA
 <213> Homo sapiens

<400> 425
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 tacagttttg tggactgagc gaggaacaa aacaaataat ttaagttggc tagagcttct 120
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 gtattttcaa agactgccac gtgccttagg aatactgttt tatctccata ctttggatga 180
 cttggt 186

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<210> 426
<211> 465
<212> DNA
<213> Homo sapiens

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<400> 426
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aaggataaagc agccaatgga tgccaaggag ttcgaacctt aagacgtatt gcccaatggg 180
gatgggacct accagggctg gataaccttg gctgtacccc ctggggaaga gcagagatat 240
acgtgccagg tggagcacc aggcctggat cagccccctca ttgtgatctg ggagccctca 300
ccgtctggca ccctagtcac tggagtcac agtggaattg ctgtttttgt cgtcatcttg 360
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<210> 427
<211> 480
<212> DNA
<213> Homo sapiens

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<400> 427
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agcttcctca gaattgtggc tgtgccacgc tggaccacag ggtccccctc aagcatctcg 180
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tgggcctggg ggccttagaa cactcctcct cctgagccta ctgccaaacg tcctcagtgt 300
tgtctgcacc tgctccgact ccttcagccg cccattcag cgcccgctcc gtccagtgcc 360
cgccctgttg ggccaaggcg gccgtgcctt actactctgt gtcttctgcc tcctctgagg 420
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<210> 428
<211> 533
<212> DNA
<213> Homo sapiens

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<400> 428
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tatttcatec ggaagccgcc aagtgatttt ctcttcccca aaccaatag gttccagcct 180
gaactgtctg cccctgatct gcggcgattt atcgatggtc caaaccgggc tgtggccctg 240
cttccggagc tacgggaggt cgtctcctct atcagctaca tcgctcgaca gctgcaggaa 300
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ctcttcctgt ggactttcat catcttcacc agcggtggga ccctagtcac cttcctggac 420
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5 gccccctgcc agttgaagtg agagagtttg gtgatactgt caagccctat cct 533

<210> 429
<211> 486
<212> DNA
10 <213> Homo sapiens

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15 cgatgttagt gtttccattg tattttcttta cagtgtgcca ttctgttaga tactatcctt 180
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acacacacac acacacacac acgcacacac acacaccaag taccagtata agcatctccc 420
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25 gcatgt 486

<210> 430
<211> 97
<212> DNA
30 <213> Homo sapiens

<400> 430
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35 ccctcagcaa ccccaggggt gtcagacggg gcaccct 97

<210> 431
<211> 241
<212> DNA
40 <213> Homo sapiens

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<222> (88)..(88)
45 <223> n is a, c, g, t or u

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50 taccaccaa cttttaaacc ctttaaaggc tcctccagtg tcagattcaa atccaacatt 180
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t 241
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<210> 432
 <211> 537
 <212> DNA
 <213> Homo sapiens

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 10 caggggtgtcg cgggtggggg gtcactgctg aggccgtgag gggaaatctgc tcaggcctgt 180
 ccctggcttc tgggggctgc tgggtgttatt ttcagttcct tgggtgtgtgg atacttcgcc 240
 ccatctctgc cttcacctgt gtcctccctg tgtgggtgct ggtgtccaaa atttcccctt 300
 15 ttcgtagtga caccagctgt gttggattgg ggcccaccct gctccagcat ggcctaattct 360
 taactaatta catttgcaag gatcttatgt ccacaaaagt cacagtctga ggtgctgggg 420
 gttaggactt caatatataa attttgcggg tacacaattc aatccatgac agaatccaaa 480
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 45 aaagangact cttgaaagtc aagtgaata ctatgcactt aaactggaac aagaatcaaa 240
 ggcttaccag aagatcaaca atgaacgccg tacataccta gctgaaatgt ctcaggggtc 300
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 ggtagacgaa tgggctgagg acacagttca tgaaagagaa atataactca gatagaagaa 180
 10 cctgcttcat cttagtgggtg atttttgtaa aatgtaattt aaaatattcc ccgatgctgg 240
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 tgtccccaca actccggagg acttcctcag caatgtggat gagatggata caggagaaaa 180
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 30 actaccattg taacttggat gtagccatga ccttacattt cctgggcctc ttggaaaaag 420
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 ggatagatca catcccagat ctcccactgc ctaaacctct gatctcttat atccgaaagt 180
 10 tctactacta tgatcctcag gaagaggtat acctgtctct aaaggaagcg cagctcattt 240
 ccaaacagaa gcaagaggtg gaaccctcca cgtagcgagg ggctccctgc tggtcaccac 300
 caagggcatt tggttgcaa gctccagctt tgaagaacca aattaagcta ccatgaaaag 360
 15 aagaggaaaa gtgagggaaac aggaaggttg ggattctctg tgcagagact ttggttcccc 420
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 30 ctgggtcaga atcccttggg gtctagtgga gtgaagatgc tgtttgaaac cttgacatgt 180
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 35 catccctggg cagaaaggcc ttcttctcat gacttcatga tctgaatccc ccgagtcac 360
 tcattctcca tgaagtcac gattttccag gtgttggtga actgcctgtg actcctctcc 420
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aaaagaaagg tggcttaaag gaactgtttg gaaagggccc tcaaaatgcc ttcttcctcg 180

taaaattctg ggctgattta aactgcaata ttcaagatga tgctggggct ttttatgggtg 240

taaccagtea gtacgagagt tctgaaaata tgacngtcac ctgnnccacc aanntttgct 300

ccnntgggaa gcnnngtagta gnnaaantag anncggagta tgcaaggtn nagaatggcc 360

gatttgtann ccgaataaac cgctcncna tgtgtgaata tatgatcnac ttcacccaca 420

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<212> DNA

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ccagaggcac ctttatcttc tgaattggac ttgcctctgg gtaccagtt atctgttgag 180

gaacagatgc caccttgga ccagactgag ttcccccca aacaggtgtt ttccaaggag 240

gaagcaagac agcccacaga aacccctgtg gccagccaga gctccgacaa gccctcaagg 300

gaccctgaga ctcccagatc ttcaggttct atgcgcaata gatggaaacc aaacagcagc 360

aaggtactag ggagatcccc cctcaccatc ctgcaggatg acaactcccc tggcaccctg 420

acactacgac agggtaagcg gccttcaccc ctaagtgaat atgttagtga actaaaggaa 480

ggagccattc ttggaactgg acgacttctg aaaactggag gacgagcatg ggagcaaggc 540

caggaccatg acaaggaaaa tcagcacttt cccttggtgg a 581

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<211> 449

<212> DNA

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 gttttttctt attacctaag caatatattt ttattatagc aacctcagaa aagaaaaata 360
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 25 caaccgtcaa ggcagcggag ctggctgtcc agaatgaagt tggcctgggt gataaccctc 300
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 cagtgtcatc ttcagaactg atgtcccaga ctccagtgga agttctgggt accaacgaga 180
 atgagaaact gagccctaca agtaatacct catatagttt agaaaaaatc tccagtctgg 240
 45 cccctcctag catggagtac tgcgttttac tcttctgtg ttgtatttgt ggttttgaat 300
 caaccagcaa agaaaacctc ttggatcata tgaaagagca cgagggtgaa attgtaaaca 360
 tcatcctgaa taaggaccac aatacagctc taaacacaaa ttaggtggaa taatgactcg 420
 50 agcaggaaag cagtagaaga ggattccttc accacagttt cacctttacg ctgtcagaca 480
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 acttcaagat taaaccaatc taaactgaat attgatgtgg acatgggggg gtgggagtag 240
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 10 tatgattatc ttttaataaan tatgtgataa aattttaaaaa aagcaaaaaca aaacttctag 360
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 25 cccctaatat gcc 133
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taacaaaagc tcgtcttttt ctgctgcagt taatacctcg gtgcccga aaagagcttct 360
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20 gaaatgaatt ctaagagtgc tccaagctcc cgaagccgaa gtctcacttt gctcccacat 180
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25 tccggccagc ttcacgaagt cagagaggta cacactctcc tgacagagga aagctgtttg 360
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<212> DNA
<213> Homo sapiens

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aaatgactgg tgtgatgttg agtaacaagt tggtagctt acttttagcta tttattaact 180
tgctcatctc atagaacatt ttaatagatt tttcacacac ctcatatta aaaaaaaca 240
aacatgctgg tgtcttggtt acccattatt cctctgtacc tgaattcagg ttggtttttc 300
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atctaccacc aaagaactca tcca 384

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aagtacctta ttctacatca ttaaccagta aggacttttt aattaaccac aataccacta 180
tcacaccta taatagtaat tccttatgga tcttttcttt agacctattt ttgaaggcat 240
aaaagcagtt gagtttctgg agaatttttg gatggtgatt aatgacttga ctggctgctc 300
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accttgtgtg ctcagatcat cttcaggaag gaaaaggcat cctggagaca ggagtccatt 120
cactcctctg ctctctaccc actcatttgc ttgccaaact tagctttgcc agtgatagtc 180
aatattaaag tgtacttttt tcccctttaa tccaatatag ttg 223

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<212> DNA
<213> Homo sapiens

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5 <400> 456
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 tcaattatatt catatgttat gttctcttca tgtgcatttt tcaatgatat attatgttcc 120
 attgtgttgg aatgtgaatg ttcaattact tttccctata 160

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 <213> Homo sapiens

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 gtgagggttg ccaaactacc gccggaggag atgggggtctc agagcgagag ctgcgagggg 180
 ggaggggaag aagaaggcct cacttttgcg gctgcggggc ccacacagcc gctgctactt 240
 20 tgggggggtg ggaaggggccc aagctgcaga cacacacagt cattcatttc tgtccacacc 300
 cctgtgggtg gcgggtgtgc gtgtgtgtgc ttgtgtgtgc gcacgtgtcg gcgctcacac 360
 acacatgcta gccactgat gcaccagcc cagggtggc agtctttgca gcgtggggcc 420
 25 gtctcaccct ggagcctgga gaggatctat gcttgtttgt ttttg 465

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 ancctccggg cctgtttcct ccctctgaag tggcgacnag tagtagaacc gacctcgtag 180
 gctcatcggg aggtcctgat gggagaaccc at 212

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gtgtaacttc tgcgtctaca aaaagaggat aggccgtcac nnctcacatg gctttgcgtg 180
10 aaagcccaat ggtactgtct ctatggcaga gatgaggaag gaacaccagc gtcctccaac 240
tttctgttc ttcctttggg ttaatggcca ctgtaaggaa acagttttct gccacgtgtg 300
gggtgatttg aatgtaaaat gcccaactct catagcaggc tg 342

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<211> 519
<212> DNA
<213> Homo sapiens
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25 aagaaatttg gacacatccc tgtctacaca ctgggctttg agagtcctca gagggatatca 180
gctgccaaaa ccgcgccaat ccagagaaga gacatctttc agtctctgca agggccacag 240
tggcagagcg tggaggaggc gttccccac atctactccc acggctgtgt cctgaaggat 300
30 gtctgcagtg agtgcaccag ctttgtggca gacgtggtgc gttccagccg caagagcgtg 360
gacgtcctca aactacgcc acgacgcagt cgccagaccc aatccctcta catccctaac 420
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35 caggccctgt atcaggctag gacgctctga gctgtgcat 519

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<212> DNA
<213> Homo sapiens
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45 tgtgtgacca tagaaagtga cgtgttaaaa accagcgtg ccctctttga aagccaggga 180
gcatcattca tttagcctgc tgagaaga 208

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<212> DNA
<213> Homo sapiens

55 <400> 462

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5 ttaaaattta aagggtcaagt aaaattgtaa atttgtaata tggaaacatt aagcgtcatt 180

atcatacaaa ttattagcag ataaccttaa taaaaataaa cgtttgctgg ttttttttga 240

gacaggggtct cgctttgtca cctaagctgg agtgcagtgc gcatctcgg ctactgcaa 300

10 cttccgcctc ctgggatcaa gtgattctcc tgccttagcc tctgagtat ctgggtttac 360

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<211> 542

<212> DNA

20 <213> Homo sapiens

<400> 463

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25 tggacaaaat ggggtgctgg gagcacatta cctgcatgga tacctccatc agagttagct 180

gcagccaacc tgagtgttga tacaacctac agacctcaca ttccaatcag caaattagtt 240

gtttcagaat cctatgatac ttatatcagt agaagtttcc aagtaacaaa agaaataata 300

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gcgtgtacct gccaaactta gggcctgtca cctcagaact ccaaggactt cgtacaaatg 420

gtccgaaaga tcccatatct gggattttgt tctgtgaag aattaggaga aactggaata 480

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<220>

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gggtggaggag gtggaggagc tgtcccccca aaactactgg cctgtggtct ggactccagg 180

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 5 ggtggaaaag gccctgccat ggggtccttg agggccagga cagcctgagg gagggatggt 360
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 <212> DNA
 <213> Homo sapiens
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 <400> 465
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 ctctggcagt ttttggtagc tcttctggat gaccgcgcaa attctcattt tattgcctgg 180
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 tatgagaaaag gaattatgca aaaggtggct ggagagagat atgtctacaa gtttgtgtgt 360
 25 gatccagaag cccttttctc catggccttt ccagataatc agcgtccact gctgaagaca 420
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 <213> Homo sapiens
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 <223> n is a, c, g, t or u
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 <223> n is a, c, g, t or u
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 ttatacccca aatcactaaa acatatagag gggctctatgt cngtttcac cataactcag 180
 ccactggtgg aacaaatctc ataataaga ggatcatagt ccctggtaag tggatccctg 240
 50 gagcattggc accatgtttt ccagtaaagt ctatctagct gtcagggaag agccacctgc 300
 nctctgcaaa gggagaggga aaatcaaac ccaggaaagg gaatatgttt ctgctccaaa 360
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 <400> 467
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 10
 <210> 468
 <211> 204
 <212> DNA
 <213> Homo sapiens
 15
 <400> 468
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 caggagttgt gagccctcta gggcaggggtg ggagccggga ccctcagggtg tagctgagct 120
 gtgacattgc tggtcatect tgggtgctctt gcttttttga aagatgcttt tttttttttt 180
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 aactgacgta gaatgaagaa ctgc 204
 <210> 469
 <211> 139
 <212> DNA
 <213> Homo sapiens
 25
 <400> 469
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 gtgattagtt tacttctagg tggaaaaaga gaggactttg aacttggtgt tgtcacagga 120
 gctgctctca tggacaaga 139
 <210> 470
 <211> 115
 <212> DNA
 <213> Homo sapiens
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 <222> (81)..(81)
 <223> n is a, c, g, t or u
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 cagcttttgag ctggaaaaac ntctgaccct ggagccaaag ccagacactg acaag 115
 <210> 471
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 <212> DNA
 <213> Homo sapiens
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 <400> 471
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 5 ccagagacca cacattgaga accactgctc tagaaaacca tttgtctttg ctgatggaga 180
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 10 gaacactctg ctagtcaagc tctctgtcac aaagacaact tgaagagaca gagtggacct 360
 cacagaagat accatcgtca ctcttaccac tgcaactgtg gtgaacagga ccactattat 420
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 <211> 446
 <212> DNA
 <213> Homo sapiens
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 <400> 472
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 ccctccacct aggctttcca ccgtggccac tccctccatg accaggcctg actctgttaa 180
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 ccttcccttc caccacacgt ggctgggcag tggttaagggt ggcaagatag tctctgtccc 360
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 <211> 443
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 <400> 473
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 45 cggcccaggg aggggtgagct ggtgcctgct ttgacgggcc aggccttggg gggcagagac 240
 aatcacgggc ggtcctgcac agattcccag gccagggtg ggtcacagga aggaaacaac 300
 attttcttga aaggggaaac gtctcccaga tcgctccctt ggctttgagg ccgaagctgc 360
 50 tgtgactgtg tcccttact gagcgcaagc cacagcctgt cttgtcaggt ggaccctgta 420
 aatacatcct ttttctgcta acc 443
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<211> 465
<212> DNA
<213> Homo sapiens

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acctccattt cccaaagtcc tctgctccag caactgccct tccaggtggg tgtgggacac 180
10 ctgggagaag gtctccaagg gaggggtgcag ccctcttgcc cgcacccctc cctgcttgca 240
cacttcccca tctttgatcc ttctgagctc cacctctggg ggctcctcct aggaaaccag 300
ctcgtgggct gggaatgggg gagagaaggg aaaagatccc caagaccccc tgggggtggga 360
15 tctgagctcc cacctccctt ccacactact gcactttccc ccttcccgcc ttccaaaacc 420
tgcttccttc agtttgtaaa gtcgggtgatt atatttttgg gggct 465

20 <210> 475
<211> 443
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<213> Homo sapiens

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gttcctaagg aaaccacctt accggggtgg aaggaggagg cagggagaag acccactctt 180
30 gctctacgag gagcaagtgc ctgccccctc ccagcagcca gccctgcaa agttgcatta 240
tctttggcca aggctgggcc tgacggttat gatttcagcc ctgggcctgc aggagaggct 300
gagaccagcc caccagcca gtggtcgagc actgccccgc cgccaaagtc tgcagaatgt 360
35 gagatgaggt tctcaaggct acaggcccca gtcccagcct gggggctggc agaggccccc 420
atatactctg ctacagctcc tat 443

40 <210> 476
<211> 458
<212> DNA
<213> Homo sapiens

45 <400> 476
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gaaactcagt ctgctggagc aggaatccca gcagcaggag ctgcagatcc agggcttcga 120
gagtgaacct gccgagatcc gcgccgaaa acagaacctg gaggccattc tgcacagcct 180
gcccagaaac tgtgccagct ggcagtgagg gctgcccaga tccccggcac aactcccc 240
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tccccgggag ccggctgctg tgaactcgac cccgtgtgga tagtcacact ccctgccgat 360
tctgtctgtg gcttcttccc tgccagcagg actgagtggt cgtaccaggt tcacctggac 420

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atgagtgcac actctcaccc ctgcacatgc ataaacgg

458

<210> 477
 <211> 475
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (342)..(342)
 <223> n is a, c, g, t or u

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 aagaaaaatg agttggtaca aaagacaaaa tcagagttca atttcagcag caagacttat 120
 caagaattta attactatgt gacatcaatg gttggttgcc tgtggacgtc caaacccctt 180
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 aacagtttaa atgtagtcca tcatccttct ttcttgagtt acgctgtttc ctttttgcta 300
 caggaaagcc cagaagaaag gacagtaaac gtgagctcta tncggggaaa gaaatggagc 360
 tggatatttg actatttatt ttacacaggg ttacaaggct tgaaactttt tataagaagt 420
 agtgttcatc attcttccat tcccagagca gagggcataa actgcaacaa tcaat 475

<210> 478
 <211> 490
 <212> DNA
 <213> Homo sapiens

<400> 478
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 <213> Homo sapiens

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 <223> n is a, c, g, t or u

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 <222> (364)..(364)
 <223> n is a, c, g, t or u

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 accctttctg tgccagttga gaatgagcct gtgtggtagc tgatgtcaga ggacaaagct 180
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 ggtggggact caggctgggt gcagcctcca aacagagaac ggaacttagg tgtgtctcta 360
 20 cagnctaggc ccagcctagc ccagcccaga acaaacaccc ttcagagcct aaccaaagaa 420
 cataagctgc aaaatgtgca cccatatttt aagctgcttt 460

25 <210> 480
 <211> 492
 <212> DNA
 <213> Homo sapiens

30 <220>
 <221> misc_feature
 <222> (77)..(77)
 <223> n is a, c, g, t or u

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 ccatccctta ctcagttgcc gggacatccc cagtctcggg ggaagaagat gccatgggct 180
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 ccctatgggtg accatctagg agaggggagg gcagaggggg tgaggggtact attctggatt 360
 45 gagaaaacct atatccattc tttatatcaa tgtatagttt tagtctccta aattgatctg 420
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 aagaacttcc ta 492

50 <210> 481
 <211> 501
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 <213> Homo sapiens

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 <223> n is a, c, g, t or u

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 <222> (247)..(247)
 <223> n is a, c, g, t or u

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 15 ggccggcagt ggccttncct cggggcccaa ggctgcagc cacctgctct aactcttgag 240
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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 <223> n is a, c, g, t or u

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 45 cntcttctat tagcacttac tgggattggt cagatagcga gtttgaatgg cagttaccag 180
 gcagntgaca ttgccagtgg gagtgatgta ctttctgatg tcatacccag tattccaagt 240
 tcaccttgcc tgcttcctaa aaagaaaaac naggaccgga atttagatga actcccttgg 300
 50 agtgcnatga canatgatga gcagggtggaa tatattgagt atctgagtcg gnnngtnant 360
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490

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 <223> n is a, c, g, t or u

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 ggctctttga ggttccctcc ttctgggtgt tcttcaggct gagcagagag gctcctgtac 180
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<210> 484
 <211> 414
 <212> DNA
 <213> Homo sapiens

<400> 484
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 aaacaggatg ttgctggagc actgtcagta gaagaaatca ctgaactact cagtctccat 360
 aaattatgct gtggccgtag ctggtatatt cagggctgtg atgctcgaag tggt 414

<210> 485
 <211> 508
 <212> DNA
 <213> Homo sapiens

<400> 485
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 gacactggct ggggccaccc cctcctgcct aatgcctcac cttacagctg gggaaactga 180
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 agctgatgcc ctgagctccc agagaggggg tgccccatct agctgggtgc aggggtcact 300
 gcttgtcagc tcagggccct gtgcccgtt gcctgttccc ctacatctgt gcctgcacat 360

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ccagaactgc ctcttgcgcg ctgcctccag gaagcccacc ttgagccaga gtcaagggct 420
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5 gggaaagctg caacctttct gttttatt 508

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10 <213> Homo sapiens

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<222> (400)..(401)
15 <223> n is a, c, g, t or u

<220>
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<222> (410)..(410)
20 <223> n is a, c, g, t or u

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25 ggaaaaaagc taattatgtc catgcctctc gtaaaactgg ggggaacctt aaagagaaaag 180
aactaaggct taagtatatc gtagtataat caattagaag taatgaatgg atgcatgtaa 240
aatggatgtg attttttttc aagcttattt tgaaatctta aaaatcaggt tacaccatag 300
30 ctactcaaaa gttttacaca cttaaaactc agatcagtaa gtgttggtac ctttttagact 360
cataaaaattg aataaaccat tgcaatgctt taaaaaaaaa naaaaaaaaa ggttttattg 420
ctatgatttt atggcagaca catccaagca aaaccatttt ccaaatgcag accttctga 480
35 tgttatctga aatctgataa aatgacccta ctctctgctg tggttcatte ttgctccatg 540
ctgtccatat ttatg 555

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40 <211> 541
<212> DNA
<213> Homo sapiens

<400> 487
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45 ctgaagggct tttttgatca gcaaaacaaa aacagaaaag caaaaaacag ttaatttttg 120
tttggccaag ttactcaac cagaccacct tgataccaac aatgctggag agcatttggc 180
aagagcaggg ccacaatgcc aaattccttg gaaaggtaga cttcctatga tactttcatg 240
50 gattggcaaa tttgtggggt ttttttggtg gtagcttttg agaatgtag tttctggctg 300
gggtagtgac ttacatctgt aatcccagca cttcgggagg cgaaggcagg tggattgctt 360
gtgccagga gtttgagacc agcctgggta acatggtgag accccatctc tatttttata 420
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aaattaaaaa aaaaaaaaaa gatagagaat gttactttcc tataaagcca tgatacccta 480
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 5 t 541

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 <212> DNA
 10 <213> Homo sapiens

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 20 <223> n is a, c, g, t or u

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 <222> (140)..(140)
 25 <223> n is a, c, g, t or u

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 catcgcaatg ctccatcaan gctagtatgt tgtgttcttt ccttcatatc aagtcaactc 180
 30 aagcttgctc tacttacctg gtgtacacag tctaagaact gtaagaagac tggagcaaaa 240
 ccactccctt gacagttgag ggtcaagctg ctctctgac tgaatttgtg accaaaagag 300
 agccactctt tttcaaccaa catctggaag ccttcaagtg tcctataaaa gggatcactg 360
 35 agtaactgaa ccagggatgt cacctagggc ataagcagga tggattgtca ttaattttag 420
 ttctgaaaaa ggcctattac taagataaaa gcacttcctt ctgatgatag ctaattcaca 480
 aattttacctg gacagcaaat ttgttacta accattccag gat 523

40 <210> 489
 <211> 306
 <212> DNA
 <213> Homo sapiens

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 50 aagtcctgt actactatat ccagcaagac actaaggggtg ctgtacctgt gtgggtggaga 180
 tggctgaagt ccgacacagc acgagcgtcc agaaatgggtg ctccccatgc ttccagctaa 240
 caggtctaga aaacccgctt gtgactagca gtccctgtgg ctgttcctgt gaggatgacg 300

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ttagca 306

5 <210> 490
 <211> 170
 <212> DNA
 <213> Homo sapiens

10 <400> 490
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 ggcgagcagg ctccagtggc aactcctgca ttacttacca gccatcggtc tctggggaac 120
 acaaggcaca agtgacaaca aaggcagaag tggagccagg cgttcacctt 170

15 <210> 491
 <211> 532
 <212> DNA
 <213> Homo sapiens

20 <400> 491
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 caccttctca aaactgagtc agcaagagaa aatcttgtct tagaagggcc agataacact 120
 tcgctgtgag aacaggaggg ataatggatt ggagatggct atgtgtaaag cagccctgcc 180
 25 tgctgattta acacactttc aaaatagatg tgtcagtatt catttaaagc aagactctga 240
 tgacagaagg aaccttgaaa actacctgat attgaaatgg ttgtgccctt tatagccctt 300
 ttgcatctcc ttgactttcc agtcatgcct cctaaatcag aagaaaagct gcaaagaaaa 360
 30 tgttttgtgt gggtctgggc ttatttgaat aatgttcatt accacaggct gccatagcac 420
 aagtgagaat ttcagaccac aagggtttaa ggagcagtgc tctcttctct caaagctcag 480
 aacgggtctct ggatccatgg tatcgtacac ccagtgtgga tattaacatt ct 532

35 <210> 492
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 <213> Homo sapiens

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 <223> n is a, c, g, t or u

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 <222> (259)..(259)
 <223> n is a, c, g, t or u

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 agcattagga atgtagcaca gttagcagat ggtgggtggc tccctctgct tttccatcag 120
 tctgtggcct agttttaaag gtgggaggaa ggggtgtgaga ttttaaggctg gttgtaaggg 180

55

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	atcagtcagt gtagttggaa aaattgtaag atgaagttat aggatataga cncaaaccctt	240
	cctggaaggc cagaaagtnt gcatagcttc aataaaggat ttggctgaaa gcagcgtaat	300
5	ccccctttacc ttgagttgat agcaatagag caaataacat gggAACgtgg gggagtttat	360
	tgaatagctt gtttactcat gtggctcctaa gaccaaccctt tgattatcca cgggtgcatg	420
	attgctctct actcgggtggc cggcaaattt aattaccac aggtgtgttg actcaaagcc	480
10	tctgtcatta aatctatgct gaataaatgc cgtcaggcca gctagtcaag gtgcacaact	540
	ctttttgtgc gtgggtgtgg	559
	<210> 493	
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	<212> DNA	
	<213> Homo sapiens	
	<400> 493	
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	tctgtaagtc tcagtgtctg cactatttgt cttggagact taaaattatc ccttgaaagc	120
	ataagaagta caccctaaac cagctttgtc cttcctgtcc tcttctagtt tacattttat	180
	gtggttagta attttgtacc taaaagtatt tgaaattcta taaatttga cttgacgtga	240
25	gcaaaaagaaa atttctacgt aagcgaaact aataaaacta cagtcac	287
	<210> 494	
30	<211> 476	
	<212> DNA	
	<213> Homo sapiens	
	<400> 494	
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	gcctggccct gggctgggca ctggggacat agcagtgacc gagacagaca ggctcacaag	120
	gagacatacg acaaccaggt aaacatggca gacaagagca tgtcagatgc gctgtgaaga	180
	acactgcggg gcccctccta ggaggtggca tgagttacat gcagacagag acgatccggg	240
40	ggcagacgga gttccatgtg gggcagtggc gagggcagac gctctggggc tgggatccct	300
	gggagtgttc gagaagcacc gagaaggctt ctgtggctgg agccggccag ctgggggaga	360
	tggggccagg gagatggcag gggcctctcc ctgtcccagg acccagagcc aaggagggt	420
45	ttaagcccag gaccaggggt ctgaaaacga aaagcactca cagtccttga acattg	476
	<210> 495	
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	<212> DNA	
	<213> Homo sapiens	
	<400> 495	
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 acgctggtgt ccacagtgtg aggacgctga ccccgggcag ccgctgctct gaagagcttc 240
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 tgtgtgtccc agccttttga gcagaaactg ccaggcagga cctgctgggc cgtgcggggc 480
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 15 gc 542

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 <211> 438
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 20 <213> Homo sapiens

 <400> 496
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 25 gagctgtatt tctatgtcac caagtaccgc caggagattc tcacggctct ggaccgagat 180
 gcctcttgtc ggaagcataa gttgcggcag aaactggaac agatcatcag cctcgtgtcc 240
 agcgacagct aaggtgggtg aatcgggtgag gagggggctt ctgagtcctg tgccgtcctc 300
 30 ccatccaggg gagtggctgg ctcaagcctg ggtccccggg ctgagccctg gattgggtat 360
 cgtggggcag gtcacctgg ccacgatgcc ccgggcacac ccaggccccc ttcatttagt 420
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 <211> 419
 <212> DNA
 40 <213> Homo sapiens

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 <400> 497
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 tgtatgaata ttcacaaatg tgcttcctta tttcagaggc tgaactaata aaaattttgt 240
 ttatttttnnn nttgaggcaa tatttttata tgggtacccta atctttaata cttaacctgc 300
 55

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cagacttttaa ccgtaacaca ataatgtatt gccaaatagc accattcttc ttctctcact 360
ctcttgccat gggggctctt aaaaaaaaaa gtatacatct aagggtgtaca acatgctgt 419

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<211> 477
<212> DNA
<213> Homo sapiens

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25 <210> 499
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<212> DNA
<213> Homo sapiens

30 <400> 499
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 tgcttacggt gaaaaatcct taagtctttg tccccgttct ctaacttcct tacgttttcg 180
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 actagggtcat taggaaaata ttaccgtcta caattttctt atactttgat ctgtctttta 300
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 gctgacattt gggcaatttg agtatgtcaa actcaataat actgggtttc atttgcaaga 240
 tccacttaaa acttaaggag gccaaaaaac atcattttaa ataccctata aattataatc 300
 atacatatga tacgaaaaat atcctacttc ag 332

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<210> 502
 <211> 375
 <212> DNA
 <213> Homo sapiens

55

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 5 aattagttga agaaaactgc aaaatatattt cttatgtaat agctgtatag agcaatagca 180
 atcaaagcat gagaaggcac taacgctggg atgaaagatg agattcagag gtgactgaga 240
 atcatgtgag tgatggctgt atattttgtg taaaatatat gtgtgaaaat gaactaagag 300
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 taaaaaccta cttga 375

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 <212> DNA
 <213> Homo sapiens

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 <223> n is a, c, g, t or u

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 gagagggttg ggggcaggag gagatttggc agtgcctgca ggtgcctgg ccagggtggag 180
 30 aggggggaaag aggaagggca ccgtgggtgt aagatgcctt tctcctccac ccatcgaaac 240
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 tcccaaattg gtgttgctgg tggacacaga tgctcccccc aatggaagcc ccaagctctg 360
 35 aggtatgcgg gtagaggctt tggatagggt ttcttctgct cccctctttt atagatctag 420
 gctgcttggc tgctgtctt tctaggcagt ccccttagag gaaaaatg 468

 <210> 504
 <211> 484
 <212> DNA
 <213> Homo sapiens

 <400> 504
 45 accccaccac gtaccagatg gatgtgaacc ccgagggcaa atacagcttt ggtgccacct 60
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 gtggggccga cagctatgag atggaggaag acggcgtccg caagtgtgag aagtgcgaag 180
 ggcttgccg caaagtgtgt aacggaatag gtattgggtg atttaaagac tcaactctcca 240
 50 taaatgctac gaatattaaa cacttcaaaa actgcacctc catcagtggc gatctccaca 300
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 55

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 20 gctttgggat cgctcnccta gcctcagaaa taattgttca agaaataaca tttctcacac 180
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 35 <223> n is a, c, g, t or u

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<213> Homo sapiens

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10 gcatggttcc catacgttt 259

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catgcaatnt aagctgcttt aagagtaacc tacaactgag gacaaatttt ctatcaactc 240
30 ccagtacccc tctctgccgt ggctgatttg ttactgggtt tcctt 285

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<400> 509
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 ggtgctctgg tctgaccgat gtgtctccca gaactattct gggggcccga caggtggggc 420
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 35 gctgtgggtct ggggtaacag cctcttccca gcacccacct gccagccctg cttgcctggc 240
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 ctacagaaac tcacagccaa atggcagagg cagggtcgct gagtctcca ggtcctgggc 180
 agccttcata tttgccattg tgtccggggc accaggagcc ccaccaacce caaacatgc 240
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 ctcacaaaaa actattttctt cagccccctt tctggcccag accctgtggg catggagatg 360
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 agaacacaac tgcaatgaca atctatgaaa accttgcgcc cgtgaccaca tttggaaaga 180

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5   tttgttctgt tttgtgagaa ctaattttga gggcatgaag ctgcatatca tagatgacaa      360
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    gaatgtggat ttttcccaca agagactttg cagggaatt tcaaggtagt gcacggaaat      180
20  atattttggg gttaaataatt ttttcccttg tctcataatg ttatgccaga gtcagattga      240
    aaagtaaata acaacatata gggcacaata aaacccatct gatgagaatg tgtggtttgt      300
    agggcatgac ttcctagacc tcttaggtag gaatctgggt aagacagaat atcagactta      360
25  gtcctcaatt cctaatagca agttctgaga tccaaaatgc tccaaaatct aaaacatttt      420
    ttagcaccga cataatgcca caagtggg                                           448

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    <213>  Homo sapiens

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    tattcaaggc cgaaacacaa gcccgaatgt ttctgtacag aaatccaatc ccatgaggat      120
    tactgagagt catgccacca agggccac                                           148

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    taaaataata agtaacattt agcatttctg accttatccc aaagtatttt aatagtatct      120
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 gggattacag ccgtcctggg ccgcccggaca ccccgctgg ggccgatgcc caacagtgcac 300
 atcgacttga gcaacctgga gcggctggag aagtaccgga gcttcgaccg ctaccggcgc 360

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 30 caagaactgc ctgcaggagc ctagtattat cctctctca 339

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 50 <211> 194
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 40 ccannnnnnn aaaaaaaaaa aananattat taacactgaa aatgcacaca tctttcaacc 480
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ctacttcaaa gcatcag 497

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aaatgcagcc agg 253

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 caatgacatc ctcaacctgg gaaacttcac tgagagcaca gatggaggaa aggccatttt 240
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Arg Thr Ser Pro Glu Gln Glu Leu Pro Ala Ala Ala Ala Pro Pro Pro
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Pro Arg Val Pro Arg Ser Ala Ser Thr Gly Ala Gln Thr Phe Gln Ser

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10	Leu	Arg	Glu	Ala	Gln	Gly	Ala	Gln	Ala	Ser	Pro	Pro	Pro	Gly	Ser	Ser	
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20	Asn	Thr	Pro	Val	Val	Gly	Trp	Val	Asn	Met	Ser	Gln	Ser	Thr	Val	Val	
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	Val	Ala	Thr	Gln	Glu	Asp	Glu	Gln	Gly	Asp	Glu	Asn	Lys	Ala	Arg	Gly	
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30	Asn	Trp	Ser	Ser	Lys	Leu	Asp	Phe	Ile	Leu	Ser	Met	Val	Gly	Tyr	Ala	
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45				260					265					270			
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		275						280					285				
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	305		310		315		320									
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10	Pro	Lys	Ile	Gln 340	Ile	Lys	Asn	Ser	Thr 345	Phe	Cys	Met	Thr	Ala 350	Tyr	Pro
15	Asn	Val	Thr 355	Met	Val	Asn	Phe	Thr 360	Ser	Gln	Ala	Asn	Lys 365	Thr	Phe	Val
20	Ser	Gly 370	Ser	Glu	Glu	Tyr	Phe 375	Lys	Tyr	Phe	Val	Leu 380	Lys	Ile	Ser	Ala
25	Gly 385	Ile	Glu	Tyr	Pro 390	Gly	Glu	Ile	Arg	Trp	Pro 395	Leu	Ala	Leu	Cys	Leu 400
30	Phe	Leu	Ala	Trp 405	Val	Ile	Val	Tyr	Ala	Ser 410	Leu	Ala	Lys	Gly	Ile 415	Lys
35	Thr	Ser	Gly 420	Lys	Val	Val	Tyr	Phe	Thr 425	Ala	Thr	Phe	Pro	Tyr 430	Val	Val
40	Leu	Val 435	Ile	Leu	Leu	Ile	Arg	Gly 440	Val	Thr	Leu	Pro	Gly 445	Ala	Gly	Ala
45	Gly	Ile 450	Trp	Tyr	Phe	Ile	Thr 455	Pro	Lys	Trp	Glu	Lys 460	Leu	Thr	Asp	Ala
50	Thr	Val 465	Trp	Lys	Asp	Ala 470	Ala	Thr	Gln	Ile	Phe 475	Phe	Ser	Leu	Ser	Ala 480
55	Ala	Trp	Gly	Gly 485	Leu	Ile	Thr	Leu	Ser	Ser 490	Tyr	Asn	Lys	Phe	His 495	Asn
	Asn	Cys	Tyr 500	Arg	Asp	Thr	Leu	Ile	Val 505	Thr	Cys	Thr	Asn	Ser 510	Ala	Thr
	Ser	Ile 515	Phe	Ala	Gly	Phe	Val	Ile 520	Phe	Ser	Val	Ile	Gly 525	Phe	Met	Ala
	Asn	Glu 530	Arg	Lys	Val	Asn	Ile 535	Glu	Asn	Val	Ala	Asp 540	Gln	Gly	Pro	Gly
	Ile	Ala 545	Phe	Val	Val	Tyr 550	Pro	Glu	Ala	Leu	Thr 555	Arg	Leu	Pro	Leu	Ser 560
	Pro	Phe	Trp	Ala	Ile	Ile	Phe	Phe	Leu	Met	Leu	Leu	Thr	Leu	Gly	Leu

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	565		570		575
5	Asp Thr Met Phe Ala Thr Ile Glu Thr Ile Val Thr Ser Ile Ser Asp	580	585		590
	Glu Phe Pro Lys Tyr Leu Arg Thr His Lys Pro Val Phe Thr Leu Gly	595	600		605
10	Cys Cys Ile Cys Phe Phe Ile Met Gly Phe Pro Met Ile Thr Gln Gly	610	615		620
	Gly Ile Tyr Met Phe Gln Leu Val Asp Thr Tyr Ala Ala Ser Tyr Ala	625	630		635
15	Leu Val Ile Ile Ala Ile Phe Glu Leu Val Gly Ile Ser Tyr Val Tyr	645	650		655
20	Gly Leu Gln Arg Phe Cys Glu Asp Ile Glu Met Met Ile Gly Phe Gln	660	665		670
	Pro Asn Ile Phe Trp Lys Val Cys Trp Ala Phe Val Thr Pro Thr Ile	675	680		685
25	Leu Thr Phe Ile Leu Cys Phe Ser Phe Tyr Gln Trp Glu Pro Met Thr	690	695		700
30	Tyr Gly Ser Tyr Arg Tyr Pro Asn Trp Ser Met Val Leu Gly Trp Leu	705	710		715
	Met Leu Ala Cys Ser Val Ile Trp Ile Pro Ile Met Phe Val Ile Lys	725	730		735
35	Met His Leu Ala Pro Gly Arg Phe Ile Glu Arg Leu Lys Leu Val Cys	740	745		750
40	Ser Pro Gln Pro Asp Trp Gly Pro Phe Leu Ala Gln His Arg Gly Glu	755	760		765
	Arg Tyr Lys Asn Met Ile Asp Pro Leu Gly Thr Ser Ser Leu Gly Leu	770	775		780
45	Lys Leu Pro Val Lys Asp Leu Glu Leu Gly Thr Gln Cys	785	790		795
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	<211> 24				
	<212> DNA				
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<220>

<223> Description of artificial sequence: Oligonucleotide

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<210> 548

<211> 21

<212> DNA

<213> artificial

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<223> Description of artificial sequence: Oligonucleotide

<400> 548

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21

<210> 549

<211> 2426

<212> DNA

<213> Homo sapiens

<400> 549

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ttgcacagag gctgagccac aggagaaagc aaagccaatg tgatttattg aatgaaagca 180

ctggacaatt accaacaact tgttcctctg ctgcctcgaa cagcataaac tggaaattgtc 240

gtgtgaaaat gacgcaacaa atgcaaaatt tacatctctg tcagtcaaaa aaacatagtg 300

ctccctcadc tcccaacgca gccaaacgcc tgtacaggaa cctctctgag aaactgaaag 360

ggagccactc ttccttcgat gaggcctatt ttaggacaag aactgatcgg ctgagtctca 420

ggaagacctc ggtgaatttc cagggcaatg aagccatgtt tgaggcagtc gaacagcagg 480

acatggatgc tgtgcagatc ctctgtatc agtacacacc agaagaactt gacctcaaca 540

cacctaacag cgagggttg acacccttg atattgccat catgaccaac aatgtgcccc 600

ttgcaaggat tcttctgagg acaggggcc gagaaagtcc acactttgtc agcctggaaa 660

gccgagcaat gcacctcaac aactggtcc aggaagccca ggagaggggtg agtgaactgt 720

ctgcccaggt ggagaatgaa ggattcactc tggacaacac agagaaagag aagcagctga 780

aagcttgagg gtggaggat cggctctaca gacgcatgaa aacaggcttt gagcatgcca 840

gagcccctga gatgccaacc aatgtctgtc tcatggtaac cagcagcaca tcaactcactg 900

tcagcttcca agagcctctt agcgtcaatg cagctgtagt aaccaggtat aaagtggaa 960

ggagtatgtc cgaagacttt tctcctttgg ctggagaaat catcatggat aatctgcaga 1020

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cttacaatat gaaaggatgg ggacctgctc agaccacgac accggcatgt gcctctcctt 1140

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<210> 550
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 40 <213> Homo sapiens
 <400> 550

Met Glu Ala Ser Leu Thr Arg Arg Leu Leu Phe Lys Asp Arg His Phe
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Thr Cys Ser Lys Ile Ile Gly Arg Arg Phe Ala Cys Phe Ala Gln Arg
 20 25 30

Leu Ser His Arg Arg Lys Gln Ser Gln Cys Asp Leu Leu Asn Glu Ser
 35 40 45

Thr Gly Gln Leu Pro Thr Thr Cys Ser Ser Ala Ala Ser Asn Ser Ile

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	Leu	Cys	Gln	Ser	Lys	Lys	His	Ser	Ala	Pro	Ser	Ser	Pro	Asn	Ala	Ala	
					85					90					95		
10	Lys	Arg	Leu	Tyr	Arg	Asn	Leu	Ser	Glu	Lys	Leu	Lys	Gly	Ser	His	Ser	
				100					105					110			
	Ser	Phe	Asp	Glu	Ala	Tyr	Phe	Arg	Thr	Arg	Thr	Asp	Arg	Leu	Ser	Leu	
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	Arg	Lys	Thr	Ser	Val	Asn	Phe	Gln	Gly	Asn	Glu	Ala	Met	Phe	Glu	Ala	
		130					135					140					
20	Val	Glu	Gln	Gln	Asp	Met	Asp	Ala	Val	Gln	Ile	Leu	Leu	Tyr	Gln	Tyr	
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25					165					170					175		
	Pro	Leu	Asp	Ile	Ala	Ile	Met	Thr	Asn	Asn	Val	Pro	Ile	Ala	Arg	Ile	
				180					185					190			
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35		210					215					220					
	Val	Ser	Glu	Leu	Ser	Ala	Gln	Val	Glu	Asn	Glu	Gly	Phe	Thr	Leu	Asp	
	225					230					235					240	
40	Asn	Thr	Glu	Lys	Glu	Lys	Gln	Leu	Lys	Ala	Trp	Glu	Trp	Arg	Tyr	Arg	
					245					250					255		
	Leu	Tyr	Arg	Arg	Met	Lys	Thr	Gly	Phe	Glu	His	Ala	Arg	Ala	Pro	Glu	
45				260					265					270			
	Met	Pro	Thr	Asn	Val	Cys	Leu	Met	Val	Thr	Ser	Ser	Thr	Ser	Leu	Thr	
			275					280					285				
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	305		310		315		320
5	Glu Ile Ile Met	Asp 325	Asn Leu Gln Thr	Leu 330	Arg Cys Thr	Ile Thr Gly	335
	Leu Thr Met Gly	Gln 340	Gln Tyr Phe	Val 345	Gln Val Ser	Ala Tyr Asn Met	350
10	Lys Gly Trp Gly	Pro 355	Ala Gln Thr	Thr 360	Thr Pro Ala	Cys Ala Ser Pro	365
15	Ser Asn Trp Lys	Asp 370	Tyr Asp Asp	Arg 375	Glu Pro Arg	His Lys Gly Gln	380
	Ser Glu Val Leu	Glu 385	Gly Leu Leu	Gln 390	Gln Val Arg	Ala Leu His Gln	400
20	His Tyr Ser Cys	Arg 405	Glu Ser Thr	Lys 410	Leu Gln Thr	Thr Gly Arg Lys	415
25	Gln Ser Val Ser	Arg 420	Ser Leu Lys	His 425	Leu Phe His	Ser Ser Asn Lys	430
	Phe Val Lys Thr	Leu 435	Lys Arg Gly	Leu 440	Tyr Ile Ala	Val Ile Phe Tyr	445
30	Tyr Lys Asp Asn	Ile 450	Leu Val Thr	Asn 455	Glu Asp Gln	Val Pro Ile Val	460
35	Glu Ile Asp Asp	Ser 465	His Thr Ser	Ser 470	Ile Thr Gln	Asp Phe Leu Trp	480
	Phe Thr Lys Leu	Ser 485	Cys Met Trp	Glu 490	Asp Ile Arg	Trp Leu Arg Gln	495
40	Ser Ile Pro Ile	Ser 500	Ser Ser Ser	Ser 505	Thr Val Leu	Gln Thr Arg Gln	510
45	Lys Met Leu Ala	Ala 515	Thr Ala Gln	Leu 520	Gln Asn Leu	Leu Gly Thr His	525
	Asn Leu Gly Arg	Val 530	Tyr Tyr Glu	Pro 535	Ile Lys Asp	Arg His Gly Asn	540
50	Ile Leu Ile Val	Thr 545	Ile Arg Glu	Val 550	Glu Met Leu	Tyr Ser Phe Phe	555
55	Asn Gly Lys Trp	Met 555	Gln Ile Ser	Lys 560	Leu Gln Ser	Gln Arg Lys Ser	565

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	565	570	575
5	Leu Ser Thr Pro Glu Glu Pro Thr 580	Ala Leu Asp Ile Leu 585	Leu Leu Ile Thr 590
	Ile Gln Asp Ile Leu Ser Tyr His Lys Arg Ser His Gln Arg Leu Phe 595	600	605
10	Pro Gly Leu Tyr Leu Gly Tyr Leu Lys Leu Cys Ser Ser Val Asp Gln 610	615	620
	Ile Lys Val Leu Val Thr Gln Lys Leu Pro Asn Ile Leu Cys His Val 625	630	635
15	Lys Ile Arg Glu Asn Asn Asn Ile Ser Arg Glu Glu Trp Glu Trp Ile 645	650	655
20	Gln Lys Leu Ser Gly Ser Glu Ser Met Glu Ser Val Asp His Thr Ser 660	665	670
	Asp Cys Pro Met Gln Leu Phe Phe Tyr Glu Leu Gln Met Ala Val Lys 675	680	685
25	Ala Leu Leu Gln Gln Ile Asn Ile Pro Leu His Gln Ala Arg Asn Phe 690	695	700
30	Arg Leu Tyr Thr Gln Glu Val Leu Glu Met Gly His Asn Val Ser Phe 705	710	715
	Leu Leu Leu Leu Pro Ala Ser Asp Asp Val Cys Thr Ala Pro Gly Gln 725	730	735
35	Asn Asn Pro Tyr Thr Pro His Ser Gly Phe Leu Asn Leu Pro Leu Gln 740	745	750
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<210> 553
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 <212> DNA
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 ttctccgcca ggcccggcgg gcgggagcgg gggcgaggga gcaggagcgg ccagtgcctc 180
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 gtcagcagcc gcctcctccc ccgcggaccg aggcggcgcc ggcgcccgga cagcccgtgg 420
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 tcaagagcct ggcgcagtcc ctgtaccctc gctccgcgca gcagctcaac gaggacctgc 540
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<210> 554
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<400> 554

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 20 25 30

Pro Pro Pro Pro Pro Arg Thr Glu Ala Ala Pro Ala Ala Gly Gln Pro
 35 40 45

Val Glu Ser Phe Pro Leu Asp Phe Thr Ala Val Glu Gly Asn Met Asp
 50 55 60

Ser Phe Met Ala Gln Val Lys Ser Leu Ala Gln Ser Leu Tyr Pro Cys
 65 70 75 80

Ser Ala Gln Gln Leu Asn Glu Asp Leu Arg Leu His Leu Leu Leu Asn
 85 90 95

Thr Ser Val Thr Cys Asn Asp Gly Ser Pro Ala Gly Tyr Tyr Leu Lys

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		130					135					140								
10	Arg	Leu	Met	Ser	Ser	Arg	Asp	Trp	Pro	Arg	Thr	Arg	Thr	Gly	Thr	Gly				
	145					150					155					160				
	Ile	Leu	Ser	Ser	Gln	Pro	Glu	Glu	Asn	Pro	Tyr	Trp	Trp	Asn	Ala	Asn				
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	Met	Val	Phe	Ile	Pro	Tyr	Cys	Ser	Ser	Asp	Val	Trp	Ser	Gly	Ala	Ser				
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	Val	Leu	Leu	Leu	Ala	Gly	Ser	Ser	Ala	Gly	Gly	Thr	Gly	Val	Leu	Leu				
	225					230					235					240				
30	Asn	Val	Asp	Arg	Val	Ala	Glu	Gln	Leu	Glu	Lys	Leu	Gly	Tyr	Pro	Ala				
					245					250					255					
	Ile	Gln	Val	Arg	Gly	Leu	Ala	Asp	Ser	Gly	Trp	Phe	Leu	Asp	Asn	Lys				
35				260					265					270						
	Gln	Tyr	Arg	His	Thr	Asp	Cys	Val	Asp	Thr	Ile	Thr	Cys	Ala	Pro	Thr				
			275					280					285							
40	Glu	Ala	Ile	Arg	Arg	Gly	Ile	Arg	Tyr	Trp	Asn	Gly	Val	Val	Pro	Glu				
		290					295					300								
	Arg	Cys	Arg	Arg	Gln	Phe	Gln	Glu	Gly	Glu	Glu	Trp	Asn	Cys	Phe	Phe				
45		305				310					315					320				
	Gly	Tyr	Lys	Val	Tyr	Pro	Thr	Leu	Arg	Cys	Pro	Val	Phe	Val	Val	Gln				
					325					330					335					
50	Trp	Leu	Phe	Asp	Glu	Ala	Gln	Leu	Thr	Val	Asp	Asn	Val	His	Leu	Thr				
				340					345					350						
	Gly	Gln	Pro	Val	Gln	Glu	Gly	Leu	Arg	Leu	Tyr	Ile	Gln	Asn	Leu	Gly				
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	Ala Cys Leu Ser His Glu Ile Ile Ile Arg Ser His Trp Thr Asp Val 385 390 395 400			
10	Gln Val Lys Gly Thr Ser Leu Pro Arg Ala Leu His Cys Trp Asp Arg 405 410 415			
15	Ser Leu His Asp Ser His Lys Ala Ser Lys Thr Pro Leu Lys Gly Cys 420 425 430			
	Pro Val His Leu Val Asp Ser Cys Pro Trp Pro His Cys Asn Pro Ser 435 440 445			
20	Cys Pro Thr Val Arg Asp Gln Phe Thr Gly Gln Glu Met Asn Val Ala 450 455 460			
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50	<210> 557 <211> 522 <212> DNA <213> Homo sapiens			
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<400> 557
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 5 attttgagct ctgcatctta acaagatgat ctgaacacct ctcttttgta tcaataaata 180
 gccctgttat tctgaagtga gaggaccaag tatagtaaaa tgctgacatc taaaactaaa 240
 taaatagaaa acaccaggcc agaactatag tcatactcac acaaaggag aaatttaaac 300
 10 tcgaaccaag caaaaggctt cacggaaata gcatggaaaa acaatgcttc cagtggccac 360
 ttcctaagga ggaacaaccc cgtctgatct cagaattggc accacgtgag cttgctaagt 420
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<210> 558
 <211> 21
 <212> DNA
 <213> artificial

<220>
 <223> Description of artificial sequence: Oligonucleotide

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 <400> 558
 actacggatt taggcaacag g 21

<210> 559
 <211> 24
 <212> DNA
 <213> artificial

30
 <220>
 <223> Description of artificial sequence: Oligonucleotide

35
 <400> 559
 gagatctcga gatctcgatc gtac 24

<210> 560
 <211> 2383
 <212> DNA
 <213> Homo sapiens

40
 <400> 560
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 caaatatgtg tttattcctg catgcgtggg ccacaggctg gtttcttggg tgcaatgaat 180
 agctgcagggt ttattagggg gtcttttttag atggatgtat gtttcccgat gtctatagaa 240
 50 cactccggac cccggagagt gaagactctg cctgtcggac ttgctttgag aagatccttc 300
 tccacctccc catggcagaa gttgcttcac agaggggaac agttttatgg atgtggctga 360
 gaccttaaac ttgaggcaac ccatctgagg tggcatccag aggagactgg ctggccccctc 420

55

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	cagggatgaa atataatcaa gcaattaacc acccccatca tcaccaagaa caacagtatc	660
	aacaagaaga acagggacaa caaaaccac ggatgaaaca ttcctttctc agctcagatc	720
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	cctgggctcg ttttctccag gaggtgcat tctgatccat aaaccttctc ctcggggttt	1080
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	agggaccggt cgtggaagg agagccatca gcagaaagag accctgagat ctctgcctgg	2280
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<210> 561
 <211> 21
 <212> DNA
 <213> artificial

<220>
 <223> Description of artificial sequence: Oligonucleotide

<400> 561
 cagagacgtt taggtaaact c 21

<210> 562
 <211> 21
 <212> DNA
 <213> artificial

<220>
 <223> Description of artificial sequence: Oligonucleotide

<400> 562
 taccaacgtg gaaattgaag c 21

<210> 563
 <211> 2336
 <212> DNA
 <213> Homo sapiens

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 gccagtgaca cgatcaatac cagggtgagc agcagaggaa gctcaggga gattatgaag 300
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 ggtccgcagt actgatgaac taatctgtca ctcaaacgt caggtctgca aaaaaaagaa 960

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	tcaaaccaac gatcagaaac tgattaactg tgtaattgaa ttgaattgaa aatcatccca	1080
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	agaaatctga tttgatttcc aaaaattgtg tgaatgaacc aagtttcttc atcttgatat	1200
	actaggcagg gagtttgttc ttccaagtac tagactgctt aattgcttgc ttgggggagg	1260
10	agaaatccta ggggaaaggc atatatgagc aatttctact ctgtgaagcc agcgctgtgt	1320
	cctgagctgg atcatggcca gaaacagaaa agtctactct tccctacagt ggaagcaact	1380
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	gtaaatacac ttatctgtgc tgtaactatt gaaatgaatc cacttcaa atgtatacca	1800
25	cctttctttt ttatatttct agatatgggt tcaatataga ctttctgact tttatgggtat	1860
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30	aattgctttt gtaatttact gacttggcat tttgaggcgt ttttaacaaa ttatgagaaa	2040
	taacaccttc agaaagcatg tgactacttt gatgcaacta ttacaatgt attcataaga	2100
	agtcattaac ctgtagagtt cttagacatg tggaaccttt aacaattata ctaaagagta	2160
35	catacaaat acagagctat gtaataataa ctaattttta atcctgacaa attagaagtt	2220
	aagcctacta tctgtaaaaa tatgtcctga ttcatttttt taagtatata cctgagcctt	2280
	taaaaagtat atgcctttac aattgatttc caataaaca tactgaataa catact	2336

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 <210> 564
 <211> 24
 <212> DNA
 <213> artificial

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 <220>
 <223> Description of artificial sequence: Oligonucleotide

<400> 564
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 <210> 565
 <211> 23
 <212> DNA
 <213> artificial

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<220>

<223> Description of artificial sequence: Oligonucleotide

<400> 565

gatagcaatt acctgtagtt agc

23

<210> 566

<211> 1187

<212> DNA

<213> Homo sapiens

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gagacagcca gaagaaaacg gcaggattag attaacctgt gattcctggc tggccacgag 180

gtcacccatg gcatggagct gcccacaacg cccttctcag catgaagcat cctgaaagat 240

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ttaattagtt aataaaatta accccatggt taaaaaaaaa aaaaaaa 1187

<210> 567

<211> 155

<212> PRT

<213> Homo sapiens

<400> 567

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Arg Ala Pro Arg Pro Pro Asp Gly Arg Gly Arg Val Arg Pro Arg Thr
 20 25 30

5 Gln Asp Gly Val Gly Asn His Thr Met Ala Arg Ile Pro Lys Thr Leu
 35 40 45

10 Lys Phe Val Val Val Ile Val Ala Val Leu Leu Pro Val Ser Pro Arg
 50 55 60

Arg Gly Pro Trp Leu Gly Lys Ser Ala Pro Gly Ala Gly Arg Gly Gln
 65 70 75 80

15 Gly Asp Gly Asp Thr Ala Gly Met Pro Gly Pro Gly His Leu Arg Pro
 85 90 95

20 Gly Met Ser Gly Gln Asp Glu Leu Ala Val Gly Val Arg Gly Arg Thr
 100 105 110

Gly Ser Pro Gly Trp Ala Gly Gly Thr Arg Pro Arg Gly Ser Arg Glu
 115 120 125

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 130 135 140

30 Ile Glu Arg Gly Arg Glu Ser Arg Trp Asn Pro
 145 150 155

35 <210> 568
 <211> 21
 <212> DNA
 <213> artificial

40 <220>
 <223> Description of artificial sequence: Oligonucleotide
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45 <210> 569
 <211> 21
 <212> DNA
 <213> artificial

50 <220>
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 agaaatcggtt ggctgagttc g 21

55 <210> 570
 <211> 857

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<212> DNA
<213> Homo sapiens

<400> 570

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aaaaaaaaa aaaaaaa 857

<210> 571
<211> 180
<212> PRT
<213> Homo sapiens

<400> 571

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Leu Ala Gly Thr Trp His Ser Met Ala Met Ala Thr Asn Asn Ile Ser
35 40 45
45 Leu Met Ala Thr Leu Lys Ala Pro Leu Arg Val His Ile Thr Ser Leu
50 55 60
50 Leu Pro Thr Pro Glu Asp Asn Leu Glu Ile Val Leu His Arg Trp Glu
65 70 75 80
Asn Asn Ser Cys Val Glu Lys Lys Val Leu Gly Glu Lys Thr Glu Asn
85 90 95

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Pro Lys Lys Phe Lys Ile Asn Tyr Thr Val Ala Asn Glu Ala Thr Leu
100 105 110

5 Leu Asp Thr Asp Tyr Asp Asn Phe Leu Phe Leu Cys Leu Gln Asp Thr
115 120 125

10 Thr Thr Pro Ile Gln Ser Met Met Cys Gln Tyr Leu Ala Arg Val Leu
130 135 140

Val Glu Asp Asp Glu Ile Met Gln Gly Phe Ile Arg Ala Phe Arg Pro
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15 Leu Pro Arg His Leu Trp Tyr Leu Leu Asp Leu Lys Gln Met Glu Glu
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Pro Cys Arg Phe
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<210> 572
<211> 21
<212> DNA
<213> artificial

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<220>
<223> Description of artificial sequence: Oligonucleotide

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<210> 573
<211> 21
<212> DNA
<213> artificial

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<220>
<223> Description of artificial sequence: Oligonucleotide

<400> 573
tagaaacggc acggctcttc c 21

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<210> 574
<211> 4415
<212> DNA
<213> Homo sapiens

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<400> 574
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gaccgaattc actaccagtc aaccacact acaagaaaca tcaaatgagt cctccaagca 180

gaaggaaccc aataccagat gaaaatccag atctccacga ggaaatgaag aacaccagaa 240

55

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	taaaacactc aaattttaag gttcgactgt gagggggaga taggggggtct cgagcaggat	1080
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	caccaatggt tctcatcagg cggcaacttc accctcacat gcctcccca tcctgctgg	1200
	tacacaagac cagcactagg ggaagcccgg agggagaatg ttaaccctg gcacttatct	1260
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 <211> 22
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 15 <213> artificial

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 <223> Description of artificial sequence: Oligonucleotide

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 <223> Description of artificial sequence: Oligonucleotide

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 30 cttcagtttg tcagagtgga c 21

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 35 <213> Homo sapiens

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5 <220>
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15 <220>
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 40 cctgacctgg aagccgatct ccaggagcta tgtcagacaa agactgggga tggatgtgaa 420
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 45 tatattagat attttacttt aaaatatctt aataaagttt taagcttttc tc 592

50 <210> 581
 <211> 21
 <212> DNA
 <213> artificial

<220>
 <223> Description of artificial sequence: Oligonucleotide

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21

<210> 582

<211> 21

<212> DNA

<213> artificial

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21

<210> 583

<211> 2514

<212> DNA

<213> Homo sapiens

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 <212> PRT
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40 <400> 584

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Lys Asn Met Glu Gly Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
 35 40 45

50 Ala Ala Ala Gly Ala Gly Gly Gly Gly Phe Pro His Pro Ala Ala Ala
 50 55 60

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10	Leu	Ala	Pro	Gly	Ala	Ala	Ser	Ala	Tyr	Ser	Ser	Ala	Pro	Gly	Glu	Ala	100	105	110	
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15	Ala	Ala	Ala	Ala	Ala	Ser	Ser	Ser	Gly	Gly	Pro	Gly	Pro	Ala	Gly	Pro	130	135	140	
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	Gln	Ser	Ser	Ser	Gly	Pro	Ala	Ala	Leu	Pro	Tyr	Gly	Tyr	Phe	Gly	Ser	165	170	175	
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30	Ser	Cys	Ala	Gln	Pro	Ala	Ser	Ala	Ala	Ala	Ala	Ala	Ala	Phe	Ala	Asp	195	200	205	
	Lys	Tyr	Met	Asp	Thr	Ala	Gly	Pro	Ala	Ala	Glu	Glu	Phe	Ser	Ser	Arg	210	215	220	
35	Ala	Lys	Glu	Phe	Ala	Phe	Tyr	His	Gln	Gly	Tyr	Ala	Ala	Gly	Pro	Tyr	225	230	235	240
40	His	His	His	Gln	Pro	Met	Pro	Gly	Tyr	Leu	Asp	Met	Pro	Val	Val	Pro	245	250	255	
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45	Met	Glu	Ser	Tyr	Gln	Pro	Trp	Ala	Leu	Pro	Asn	Gly	Trp	Asn	Gly	Gln	275	280	285	
50	Met	Tyr	Cys	Pro	Lys	Glu	Gln	Ala	Gln	Pro	Pro	His	Leu	Trp	Lys	Ser	290	295	300	
	Thr	Leu	Pro	Asp	Val	Val	Ser	His	Pro	Ser	Asp	Ala	Ser	Ser	Tyr	Arg	305	310	315	320

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Arg Gly Arg Lys Lys Arg Val Pro Tyr Thr Lys Val Gln Leu Lys Glu
325 330 335

5 Leu Glu Arg Glu Tyr Ala Thr Asn Lys Phe Ile Thr Lys Asp Lys Arg
340 345 350

10 Arg Arg Ile Ser Ala Thr Thr Asn Leu Ser Glu Arg Gln Val Thr Ile
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15 Lys Thr Thr Ser
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<211> 24
20 <212> DNA
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<220>
<223> Description of artificial sequence: Oligonucleotide

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<210> 586
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<220>
<223> Description of artificial sequence: Oligonucleotide

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40 <212> DNA
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15	Gln Ala Val Gln Glu Arg Phe Asn Gln Asn Lys Thr Thr Asp Pro Lys 305 310 315 320		
	Glu Glu Ile Lys Gln Val Ser Glu Asp Asp Phe Ser Lys Leu Gln Leu 325 330 335		
20	Lys Glu Ser Met Ile Pro Ile Thr Arg Ser Leu Gln Lys Ala Leu His 340 345 350		
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Tyr Phe Thr Gln Arg Arg Ala Pro Ser Thr Gly Ile His Gln Arg Ser
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Ile Ala Ser Phe Phe Thr Leu Gln Pro Gly Lys Thr Asn Gly Ser Asp
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Gln Lys Ser Val Ser Ser His Thr Glu Ser Gln Ile Asn Lys Glu Ser
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Lys Lys Asn Ala Thr Gln Leu Asp His Leu Ile Pro Gly Leu Ala His
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Asp Cys Met Ala Ser Pro Leu Ala Thr Ser Thr Thr Ala Asp Ile Gln
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Glu Ala Gly Leu Ser Pro Gln Ser Leu Gln Thr Ser Gly His His Arg
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Pro Asp Cys Ala Gly Asp Ser His Thr Pro Leu Ala Phe Ser Phe Thr
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Asp Ser Ala Arg Lys Trp Glu Trp Leu His Glu Ser Lys Lys Asn Tyr

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	Glu Asn Ile Glu Ser Val Lys Gln Ser Arg Ser Pro Val Ser Val Phe			
15		260	265	270
	Ser Trp Asp Asn Glu Lys Asn Asp Lys Asp Ser Trp Ser Gln Leu Phe			
		275	280	285
20	Thr Glu Asp Ser Gln Gly Gln Arg Val Ile Ala His Asn Thr Arg Ala			
	290	295	300	
	Pro Phe Gln Asp Val Thr Asn Asn Trp Asn Trp Asp Leu Gly Pro Phe			
25	305	310	315	320
	Pro Asn Ser Pro Trp Ala Gln Cys Gln Glu Asp Gly Pro Thr Gln Asn			
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35 40 45

15 Glu Phe Ser Arg Val Arg Glu Phe Val Gly Gln Leu Val Ala Pro Leu
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20 Pro Leu Gly Thr Gly Ala Leu Arg Ala Ser Leu Val His Val Gly Ser
65 70 75 80

Arg Pro Tyr Thr Glu Phe Pro Phe Gly Gln His Ser Ser Gly Glu Ala
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30 Thr Gly Leu Ala Leu Val Tyr Ala Lys Glu Gln Leu Phe Ala Glu Ala
115 120 125

Ser Gly Ala Arg Pro Gly Val Pro Lys Val Leu Val Trp Val Thr Asp
130 135 140

35 Gly Gly Ser Ser Asp Pro Val Gly Pro Pro Met Gln Glu Leu Lys Asp
145 150 155 160

40 Leu Gly Val Thr Val Phe Ile Val Ser Thr Gly Arg Gly Asn Phe Leu
165 170 175

Glu Leu Ser Ala Ala Ala Ser Ala Pro Ala Glu Lys His Leu His Phe
180 185 190

45 Val Asp Val Asp Asp Leu His Ile Ile Val Gln Glu Leu Arg Gly Ser
195 200 205

50 Ile Leu Asp Ala Met Arg Pro Gln Gln Leu His Ala Thr Glu Ile Thr
210 215 220

Ser Ser Gly Phe Arg Leu Ala Trp Pro Pro Leu Leu Thr Ala Asp Ser
225 230 235 240

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Gly Tyr Tyr Val Leu Glu Leu Val Pro Ser Ala Gln Pro Gly Ala Ala
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 Glu Ala Gly Pro Gly Ala Ser Gly Pro Glu Ser Gly Ala Gly Pro Ala
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 Pro Thr Gln Leu Ala Ala Leu Pro Ala Pro Glu Glu Ala Gly Pro Glu
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 20 25 30
 35 Pro Leu Gly Asp Phe Arg His Thr Ile His Ile Gly Ser Gly Gly Gly
 35 40 45
 Ser Asp Met Phe Gly Asp Ile Ser Phe Leu Gln Gly Lys Phe His Leu
 50 55 60
 40 Leu Pro Gly Thr Met Val Glu Gly Pro Glu Glu Asp Gly Thr Phe Asp
 65 70 75 80
 45 Leu Pro Phe Gln Phe Thr Arg Thr Ala Thr Val Cys Gly Arg Glu Leu
 85 90 95
 Pro Asp Gly Pro Ser Pro Leu Leu Lys Asn Ala Ile Ser Leu Pro Val
 100 105 110
 50 Ile Gly Gly Pro Gln Ala Leu Thr Leu Pro Thr Ala Gln Ala Pro Pro
 115 120 125

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Lys Pro Pro Arg Leu His Leu Glu Thr Pro Gln Pro Ser Pro Gln Glu
 130 135 140

5 Gly Gly Ser Val Asp Ile Trp Arg Ile Pro Glu Thr Gly Ser Pro Asn
 145 150 155 160

Ser Gly Leu Thr Pro Glu Ser Gly Ala Glu Glu Pro Phe Leu Ser Asn
 165 170 175

10 Ala Ser Ser Leu Leu Ser Leu His Val Asp Leu Gly Pro Ser Ile Leu
 180 185 190

15 Asp Asp Val Leu Gln Ile Met Asp Gln Asp Leu Asp Ser Met Gln Ile
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Pro Thr
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 <212> DNA
 <213> artificial

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<220>
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 <212> DNA
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 cacaggctac tgcgatgagg attgtctgaa ggggaacaaa ggccaagatg ttgtttgaag 180
 ccgtgagact gagtgagatc atggaggaag tgaatgtaaa tagaaaaggg aagaagtctg 240
 aagacggagc cctgagacac tccattgtaa actggaagat gaggaagagc cagcaaaggaa 300

50

55

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gactgagaag gggcagccag tgaagatgga gccagggcta gagtaagagc cccttctggg 360
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 5 gaacttccta cactgagaca actccagtgg aactctgata attatcctaa aataaggagg 480
 cttcttcagt agccctcgaa atatgttcaa atacatgatt acatttatgt ccttaatat 540
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 10 cagggttaatt caatgccaga gtaacttctc agaggggtgta tattcagtgt gaacaatttt 660
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<210> 612
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 50 gggcgcggct ccgagtgag cccaccaaga aggaagcggc ctgcagaggt gccgacatgg 180
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 <212> PRT
 <213> Homo sapiens

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30 Ser Ser Ser Ser Ser His Asp Glu Ala Pro Val Leu Asn Asp Lys His
 20 25 30

35 Leu Asp Val Pro Asp Ile Ile Ile Thr Pro Pro Thr Pro Thr Gly Met
 35 40 45

40 Met Leu Pro Arg Asp Leu Gly Ser Thr Val Trp Leu Asp Glu Thr Gly
 50 55 60

45 Ser Cys Pro Asp Asp Gly Glu Ile Asp Pro Glu Ala
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55 <220>
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<223> Description of artificial sequence: Oligonucleotide

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<211> 432

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ttctgccact agtctgaatt tcatgagaag atgccgattt ggctcctgtg ggctcctcagc 360

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caccaaagat at 432

<210> 618

<211> 21

<212> DNA

<213> artificial

<220>

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<212> DNA

<213> artificial

<220>

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<210> 620

<211> 2575

<212> DNA

<213> Homo sapiens

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	gaggccccca	tcctctctca	agagcatccg	attcatcgtg	ttcaaccctt	cctttgtctt	1980

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<212> PRT
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<400> 621

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30 Ala Val Leu Thr Ile Thr Phe Gly Leu Ser Ala Leu Asn Arg Phe Gln
35 40 45

35 Pro Glu Gly Asp Leu Glu Arg Leu Val Ala Pro Ser His Ser Leu Ala
50 55 60

Lys Ile Glu Arg Ser Leu Ala Ser Ser Leu Phe Pro Leu Asp Gln Ser
65 70 75 80

40 Lys Ser Gln Leu Tyr Ser Asp Leu His Thr Pro Gly Arg Tyr Gly Arg
85 90 95

45 Val Ile Leu Leu Ser Pro Thr Gly Asp Asn Ile Leu Leu Gln Ala Glu
100 105 110

Gly Ile Leu Gln Thr His Arg Ala Val Leu Glu Met Lys Asp Gly Arg
115 120 125

50 Asn Ser Phe Ile Gly His Gln Leu Gly Gly Val Val Glu Val Pro Asn
130 135 140

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	Ser	Lys	Asp	Gln	Arg	Val	Lys	Ser	Ala	Arg	Ala	Ile	Gln	Ile	Thr	Tyr	145	150	155	160
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	Trp	Glu	Asn	Glu	Phe	Cys	Lys	Leu	Ile	Arg	Lys	Leu	Gln	Glu	Glu	His	180	185	190	
10	Gln	Glu	Leu	Gln	Leu	Tyr	Ser	Leu	Ala	Ser	Phe	Ser	Leu	Trp	Arg	Asp	195	200	205	
15	Phe	His	Lys	Thr	Ser	Ile	Leu	Ala	Arg	Ser	Lys	Val	Leu	Val	Ser	Leu	210	215	220	
	Val	Leu	Ile	Leu	Thr	Thr	Ala	Thr	Leu	Ser	Ser	Ser	Met	Lys	Asp	Cys	225	230	235	240
20	Leu	Arg	Ser	Lys	Pro	Phe	Leu	Gly	Leu	Leu	Gly	Val	Leu	Thr	Val	Cys	245	250	255	
25	Ile	Ser	Ile	Ile	Thr	Ala	Ala	Gly	Ile	Phe	Phe	Ile	Thr	Asp	Gly	Lys	260	265	270	
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30	Thr	Lys	Gly	Val	Phe	Glu	Leu	Leu	Ser	Gly	Trp	Arg	Arg	Thr	Lys	Glu	290	295	300	
35	Asn	Leu	Pro	Phe	Lys	Asp	Arg	Ile	Ala	Asp	Ala	Tyr	Ser	Asp	Val	Met	305	310	315	320
	Val	Thr	Tyr	Thr	Met	Thr	Ser	Ser	Leu	Tyr	Phe	Ile	Thr	Phe	Gly	Met	325	330	335	
40	Gly	Ala	Ser	Pro	Phe	Thr	Asn	Ile	Glu	Ala	Val	Lys	Val	Phe	Cys	Gln	340	345	350	
45	Asn	Met	Cys	Val	Ser	Ile	Leu	Leu	Asn	Tyr	Phe	Tyr	Ile	Phe	Ser	Phe	355	360	365	
	Phe	Gly	Ser	Cys	Leu	Val	Phe	Ala	Gly	Gln	Leu	Glu	Gln	Asn	Arg	Tyr	370	375	380	
50	His	Ser	Ile	Phe	Cys	Cys	Lys	Ile	Pro	Ser	Ala	Glu	Tyr	Leu	Asp	Arg	385	390	395	400

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5	Ser	His	His	Glu	Thr	Asn	Pro	Tyr	Gln	His	His	Phe	Ile	Gln	His	Phe	
				420					425					430			
	Leu	Arg	Glu	His	Tyr	Asn	Glu	Trp	Ile	Thr	Asn	Ile	Tyr	Val	Lys	Pro	
10			435					440					445				
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		450					455					460					
15	Cys	Leu	Gln	Ile	Ser	Asp	Gly	Ala	Asn	Ile	Ile	Asn	Leu	Leu	Ala	Ser	
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	Trp Asn Val Asp Met Asp Cys Ile Ser Ile Leu Cys Leu Ile Tyr Thr	
10	690 695 700	
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	705 710 715 720	
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	Asp His Gly Thr Ala Ile Leu Gln Asn Val Thr Ser Phe Leu Ile Gly	
20	740 745 750	
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	755 760 765	
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Claims

1. A pharmaceutical composition, comprising one or more components selected from the group consisting of:

- (i) a tumor-associated antigen or a part thereof,
- (ii) a nucleic acid which codes for a tumor-associated antigen or a part thereof,
- (iii) an antibody which binds to a tumor-associated antigen or a part thereof,
- (iv) an antisense nucleic acid which hybridizes specifically with a nucleic acid coding for a tumor-associated antigen,
- (v) an siRNA directed against a nucleic acid coding for a tumor-associated antigen,
- (vi) a host cell which expresses a tumor-associated antigen or a part thereof, and
- (vii) isolated complexes between a tumor-associated antigen or a part thereof and an MHC molecule, said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 44, 541, 1-43, 45-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

2. The pharmaceutical composition as claimed in claim 1, in which the host cell additionally expresses an MHC molecule which binds to the tumor-associated antigen or the part thereof.

3. The pharmaceutical composition as claimed in claim 1 or 2, in which the host cell is an antigen-presenting cell.

4. The pharmaceutical composition as claimed in claim 1, in which the antibody is a monoclonal, chimeric or humanized antibody, or is a fragment of an antibody.

5. The pharmaceutical composition as claimed in claim 1 or 4 in which the antibody is coupled to a therapeutic or diagnostic agent.

6. The pharmaceutical composition as claimed in any of claims 1-5 for use in the treatment or prevention of cancer.

7. The pharmaceutical composition as claimed in claim 6, in which the cancer is a lung tumor, a breast tumor, a prostate tumor, a melanoma, a colon tumor, a gastric tumor, a pancreatic tumor, an ENT tumor, an ovarian tumor, a colorectal tumor, a cervical carcinoma, a colon carcinoma or a mammary carcinoma.

8. A method of diagnosing or monitoring a cancer disease, which method comprises detecting or determining the quantity

- (i) of a tumor-associated nucleic acid or of a part thereof, and/or

- (ii) of a tumor-associated antigen or of a part thereof, and/or
- (iii) of an antibody to the tumor-associated antigen or a part thereof and/or
- (iv) of T lymphocytes which are specific to the tumor-associated antigen or to a part thereof in a biological sample isolated from a patient, said tumor-associated nucleic acid being selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 44, 541, 1-43, 45-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
 - (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
 - (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
 - (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c), and
- said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from said group of nucleic acids.

9. Cytolytic or cytokine-releasing T cells for use in a method of treating a patient having a disease **characterized by** expression or abnormal expression of a tumor-associated antigen, which method comprises:

- (i) providing a sample containing immunoreactive cells,
 - (ii) contacting said sample with a host cell expressing said tumor-associated antigen or a part thereof, under conditions which favor production of cytolytic or cytokine-releasing T cells against said tumor-associated antigen or said part thereof, and
 - (iii) introducing the cytolytic or cytokine-releasing T cells into the patient in an amount suitable for lysing cells expressing the tumor-associated antigen or a part thereof,
- said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from the group consisting of:

- (a) a nucleic acid which comprises nucleic acid sequence selected from the group consisting of SEQ ID NOs: 44, 541, 1-43, 45-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 91, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

10. The cytolytic or cytokine-releasing T cells as claimed in claim 9, in which the host cell recombinantly or endogenously expresses an MHC molecule binding to the tumor-associated antigen or to a part thereof.

11. An antibody, which binds specifically to a protein or polypeptide or to a part thereof, said protein or polypeptide being encoded by a nucleic acid selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 44, 541, 1-43, 45-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c).

12. The antibody as claimed in claim 11, in which the antibody is a monoclonal, chimeric or humanized antibody, or is a fragment of an antibody.

13. A conjugate between an antibody as claimed in claim 11 or 12 and a therapeutic or diagnostic agent.

14. A kit for detecting cancer, which kit comprises agents for detecting or determining the quantity

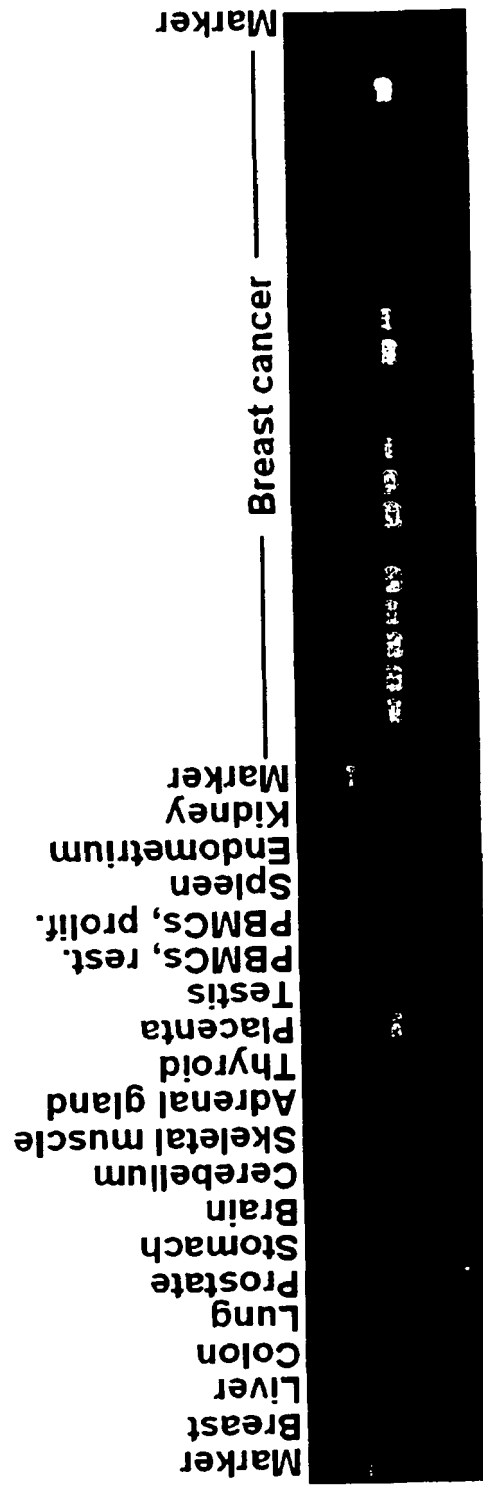
- (i) of a tumor-associated nucleic acid or of a part thereof, and/or
- (ii) of a tumor-associated antigen or of a part thereof, and/or
- (iii) of antibodies which bind to the tumor-associated antigen or to a part thereof, and/or
- (iv) of T cells which are specific for a complex between the tumor-associated antigen or a part thereof and an MHC molecule,

said tumor-associated nucleic acid being selected from the group consisting of:

- (a) a nucleic acid which comprises a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 44, 541, 1-43, 45-540, 545, 549, 553, 557, 560, 563, 566, 570, 574, 577, 580, 583, 587, 591, 595, 599, 602, 606, 610, 613, 617, 620, and 624, a part or derivative thereof,
- (b) a nucleic acid which hybridizes with the nucleic acid of (a) under stringent conditions,
- (c) a nucleic acid which is degenerate with respect to the nucleic acid of (a) or (b), and
- (d) a nucleic acid which is complementary to the nucleic acid of (a), (b) or (c), and said tumor-associated antigen having a sequence encoded by a nucleic acid which is selected from said group of nucleic acids.

Fig. 1

RT-PCR



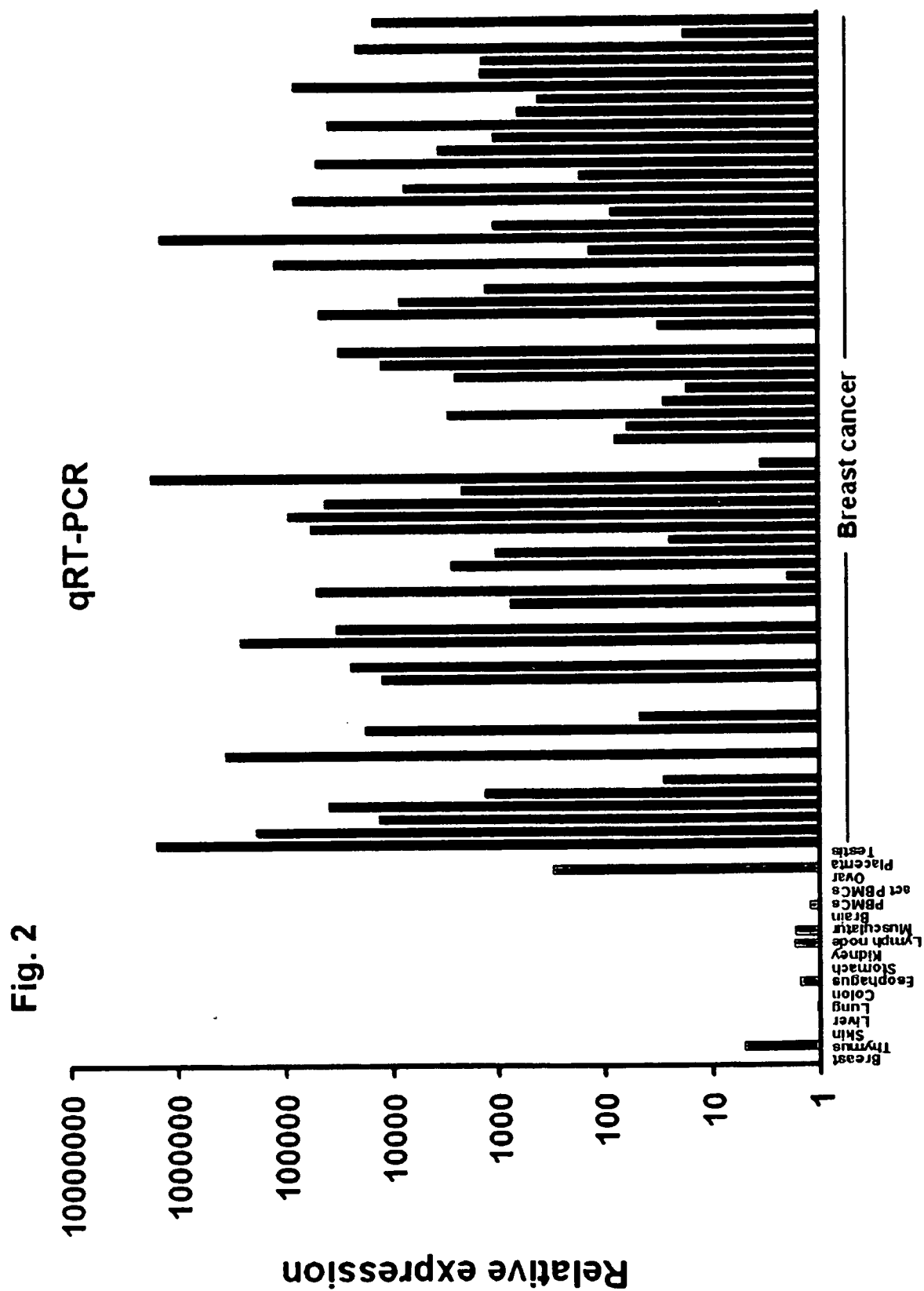
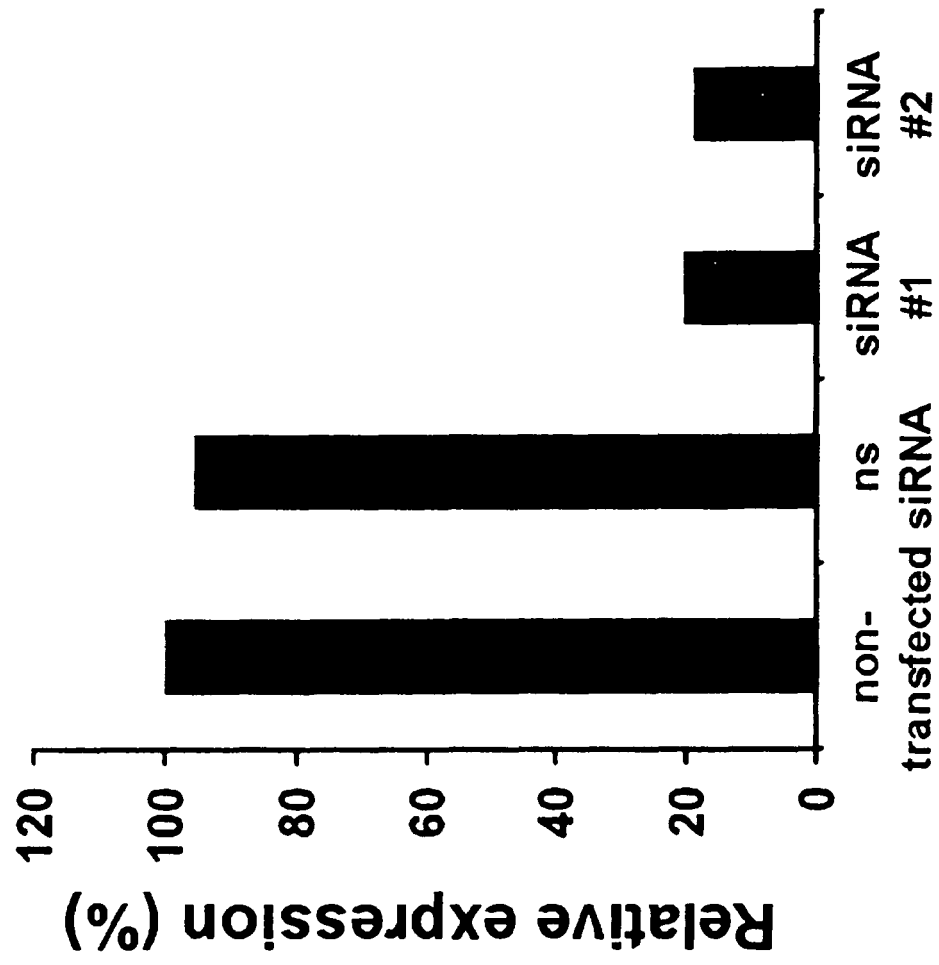


Fig. 3



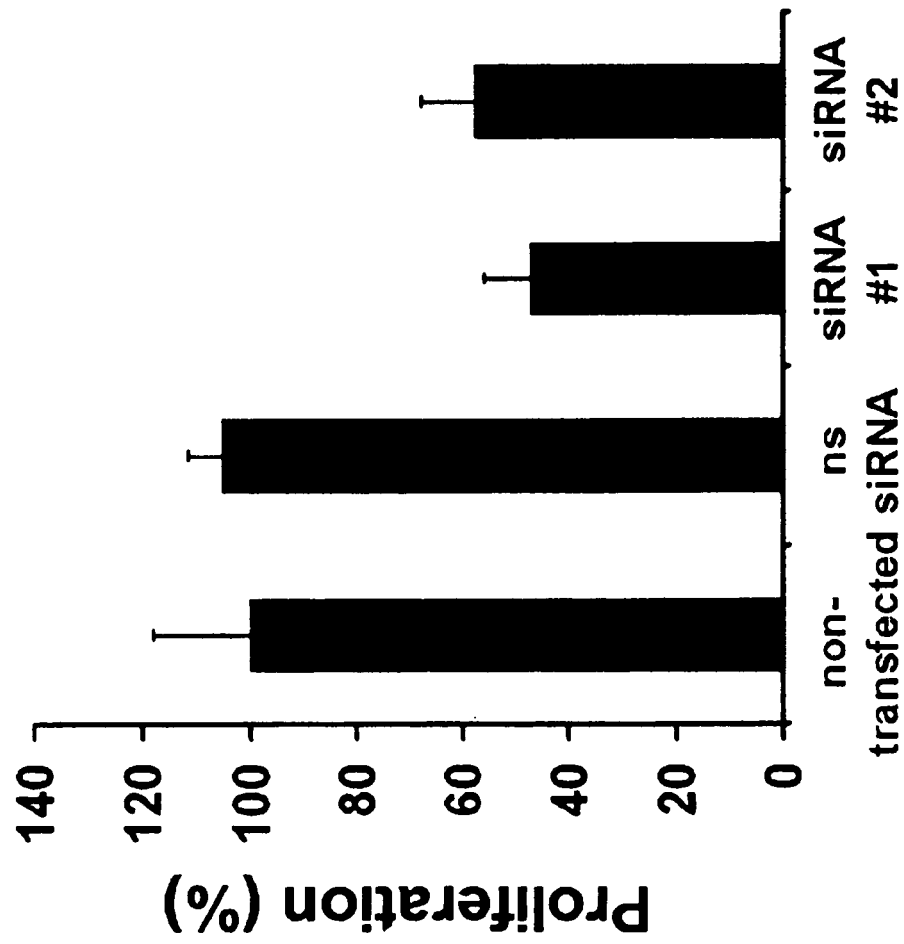


Fig. 4

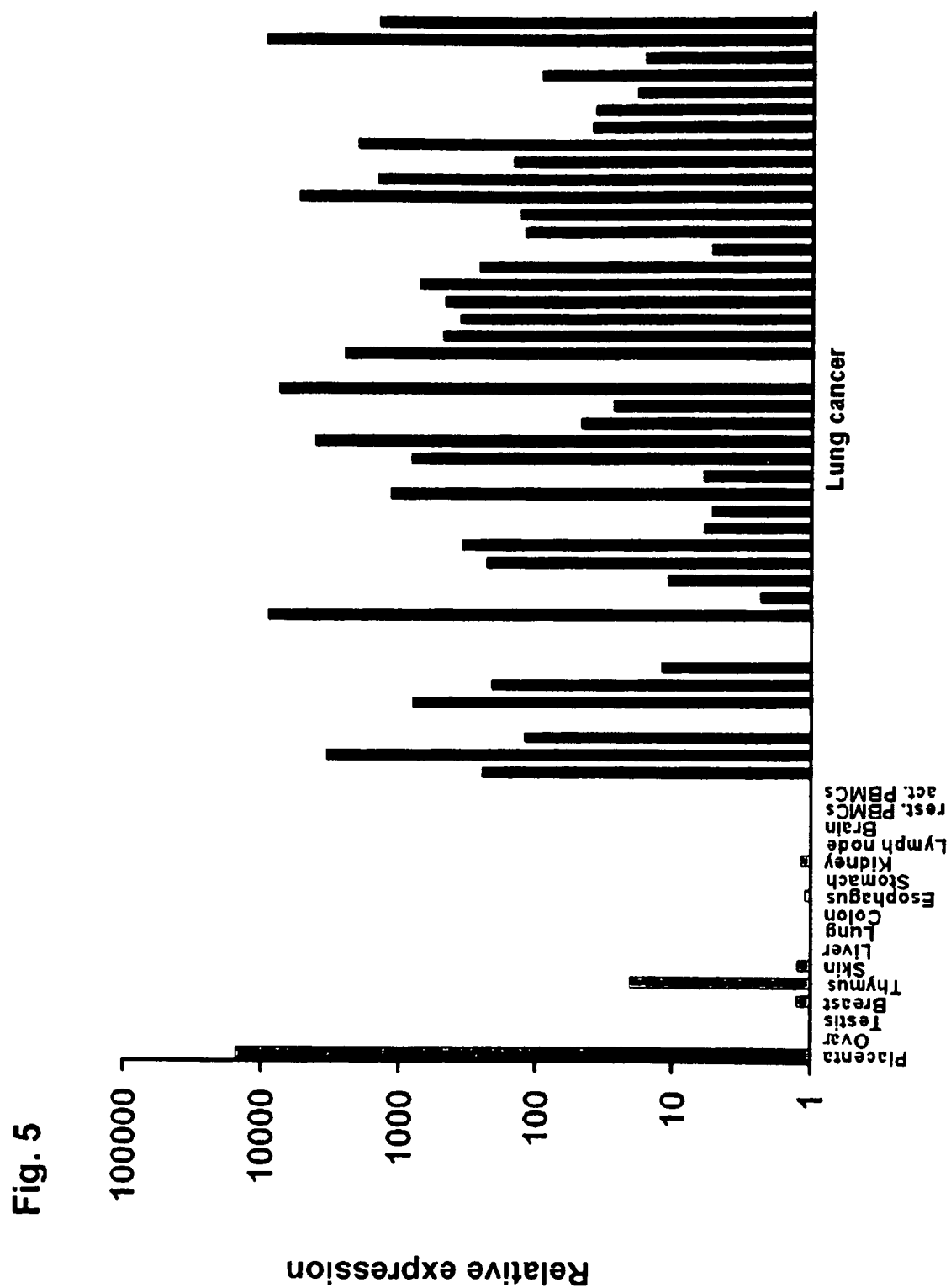
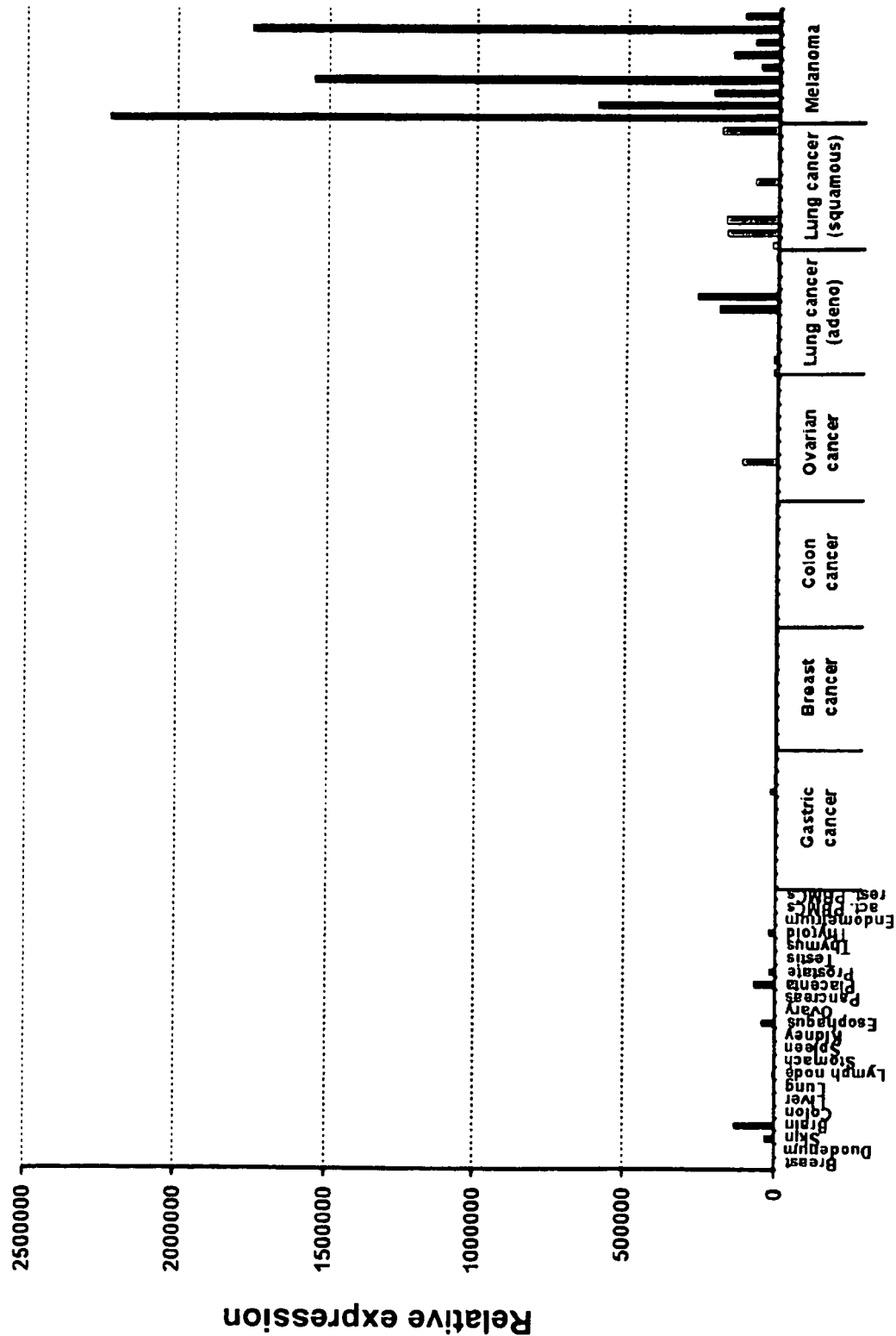


Fig. 6



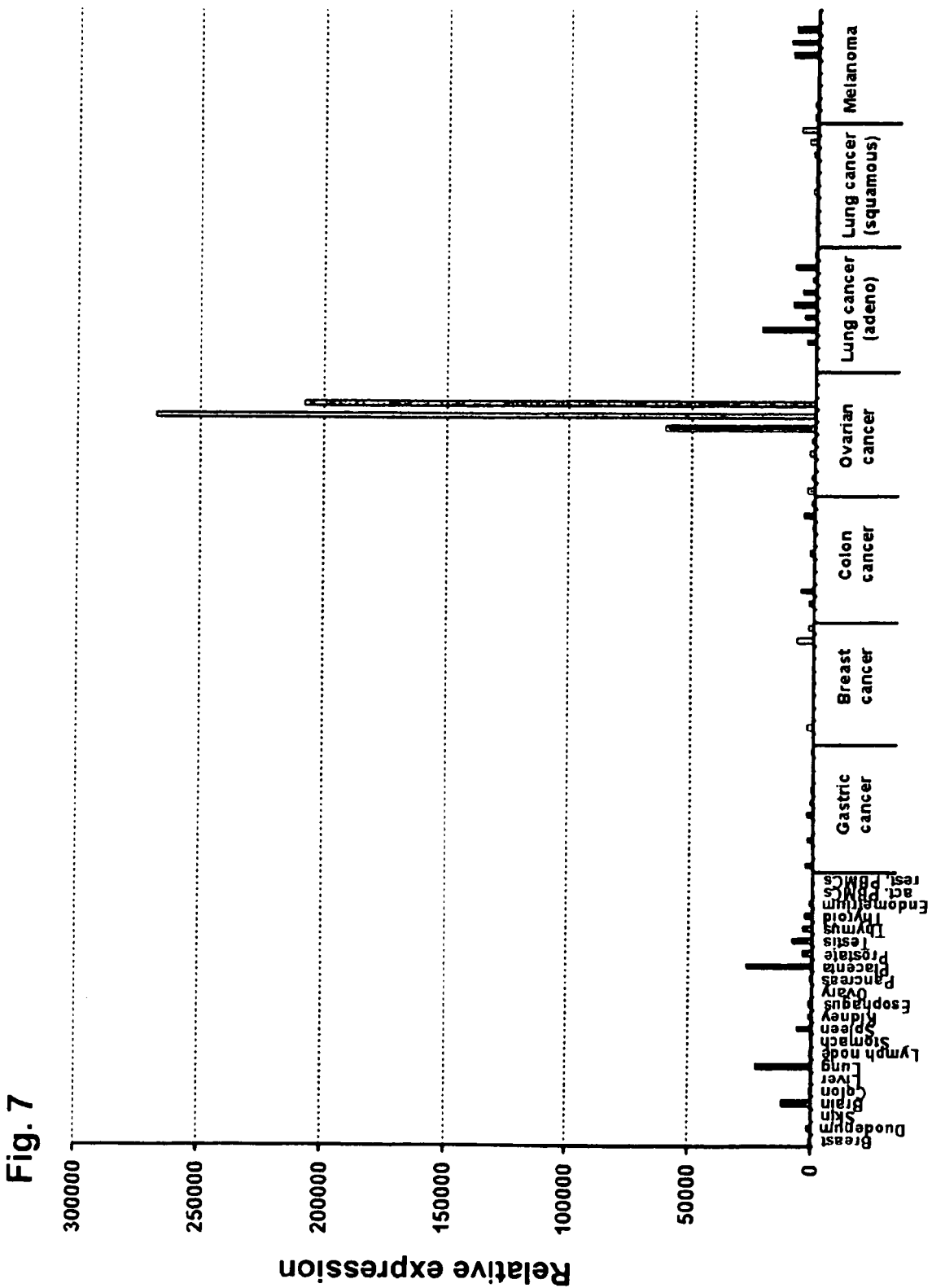
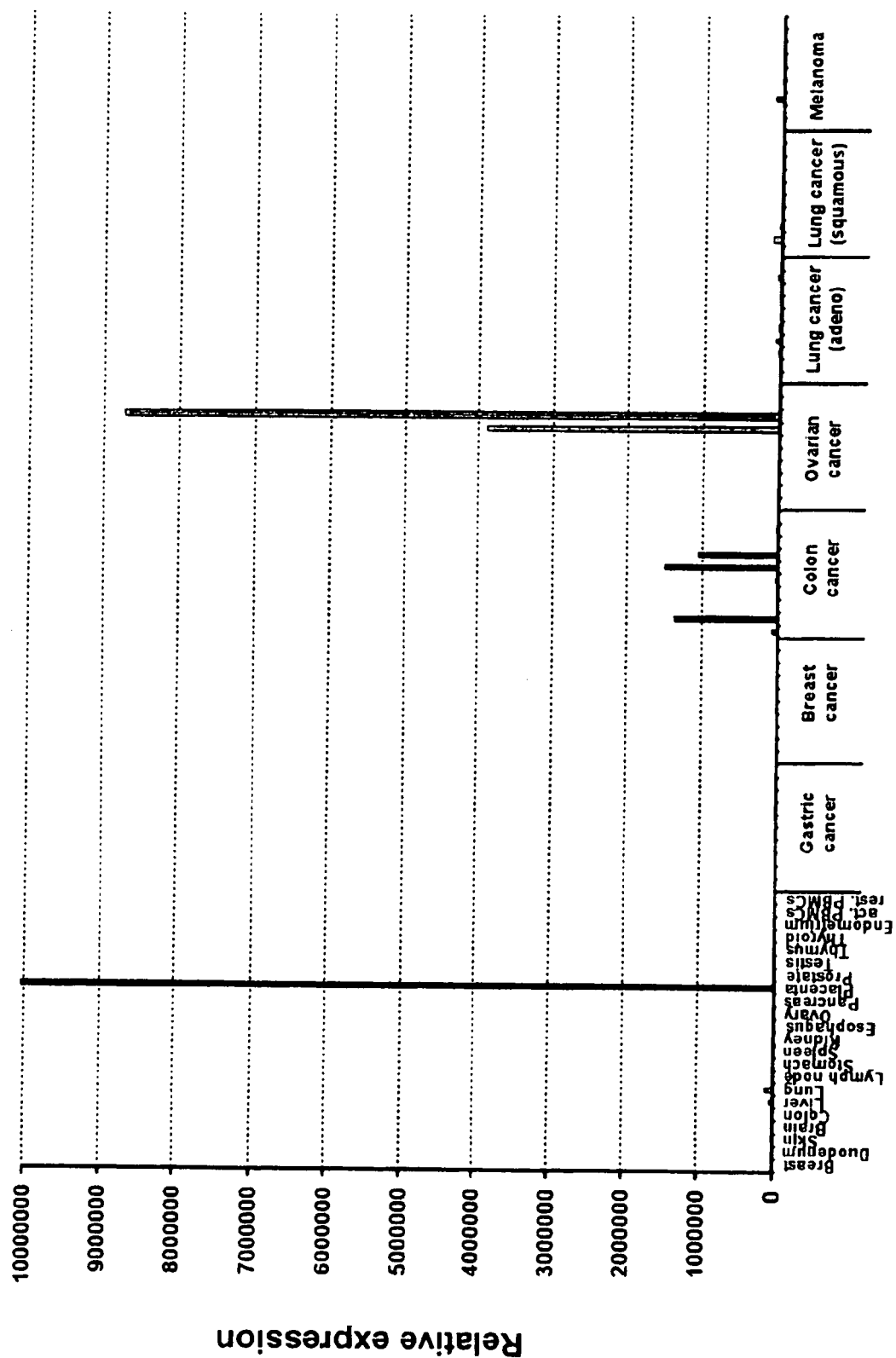
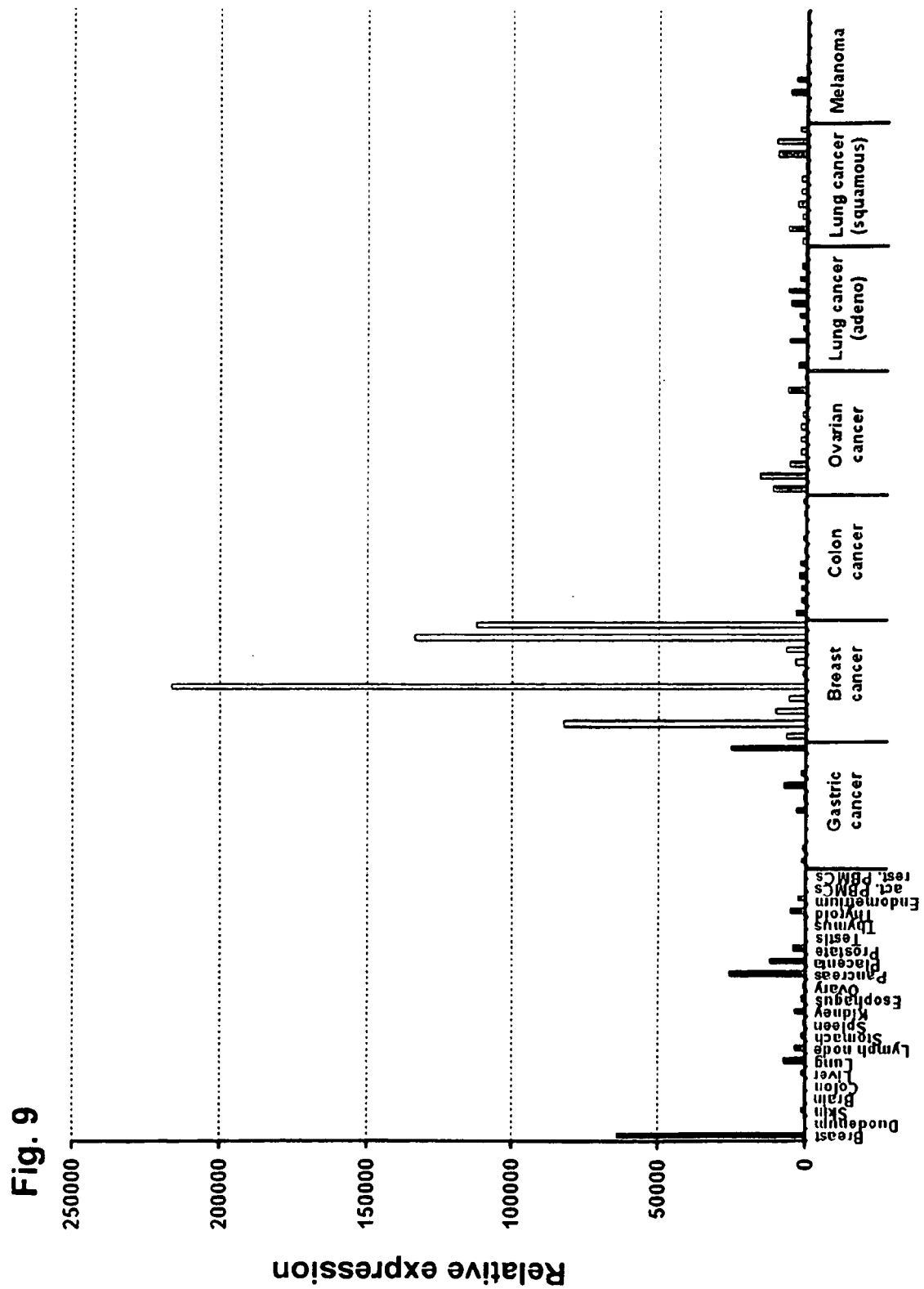


Fig. 8





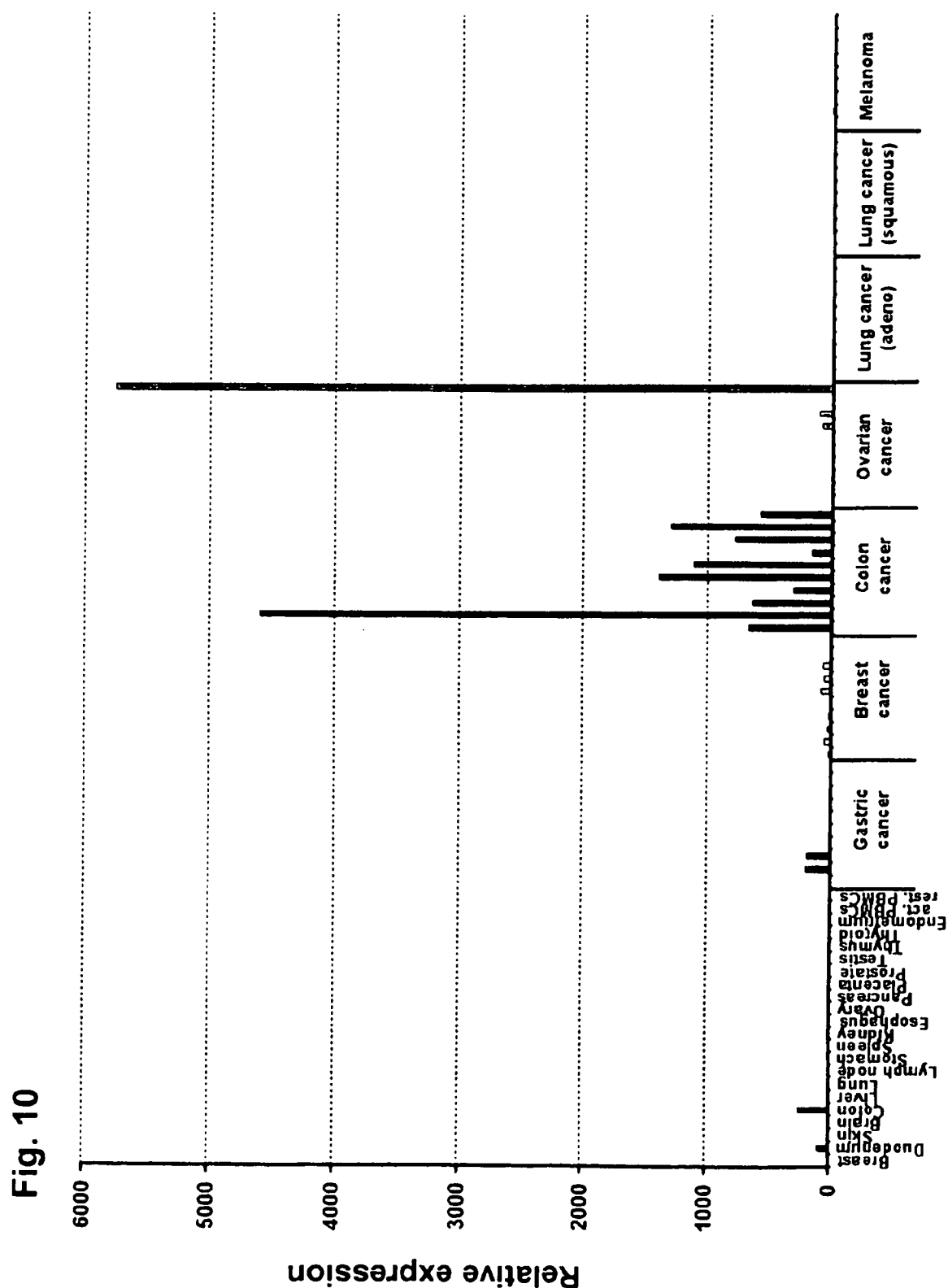


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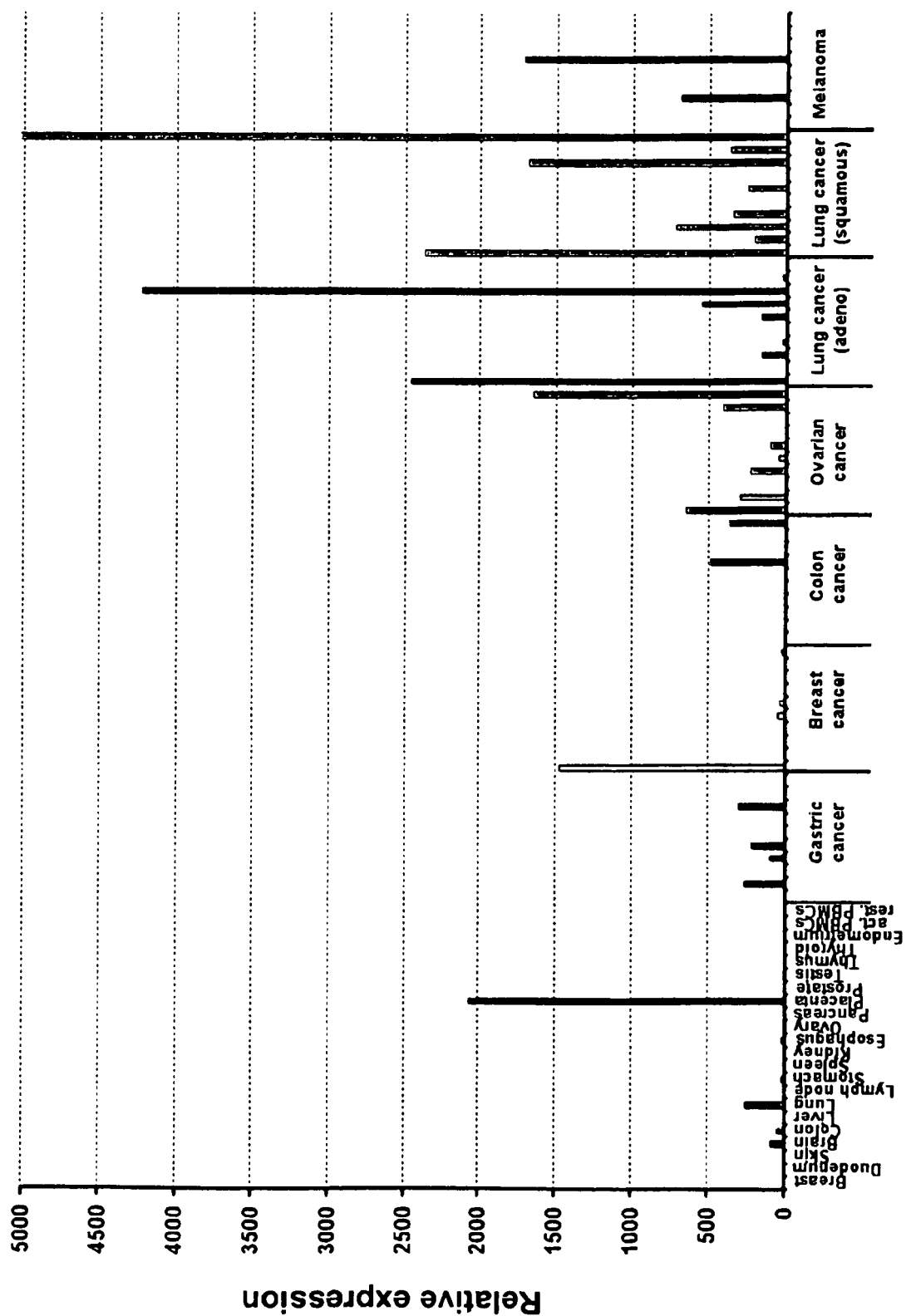


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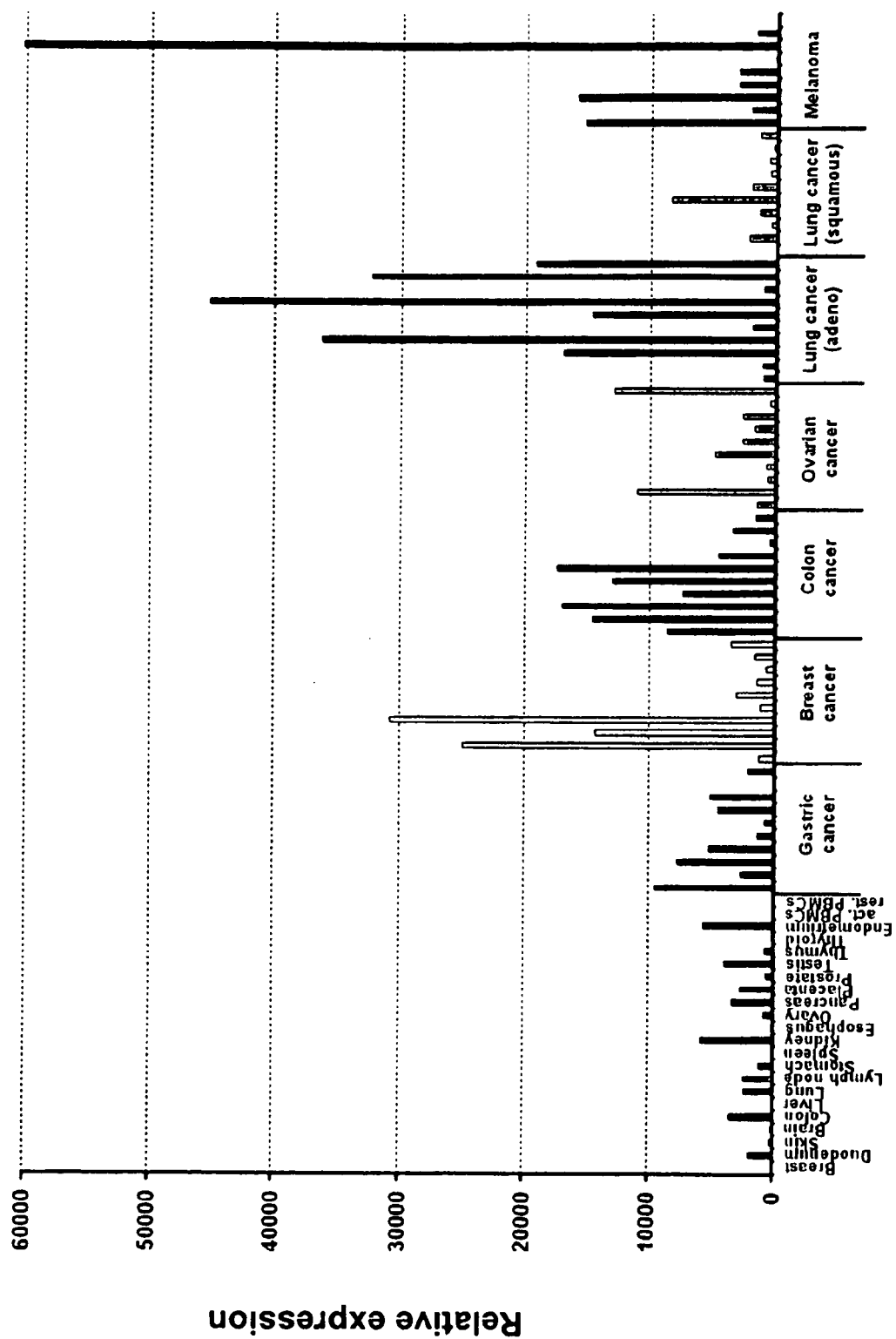


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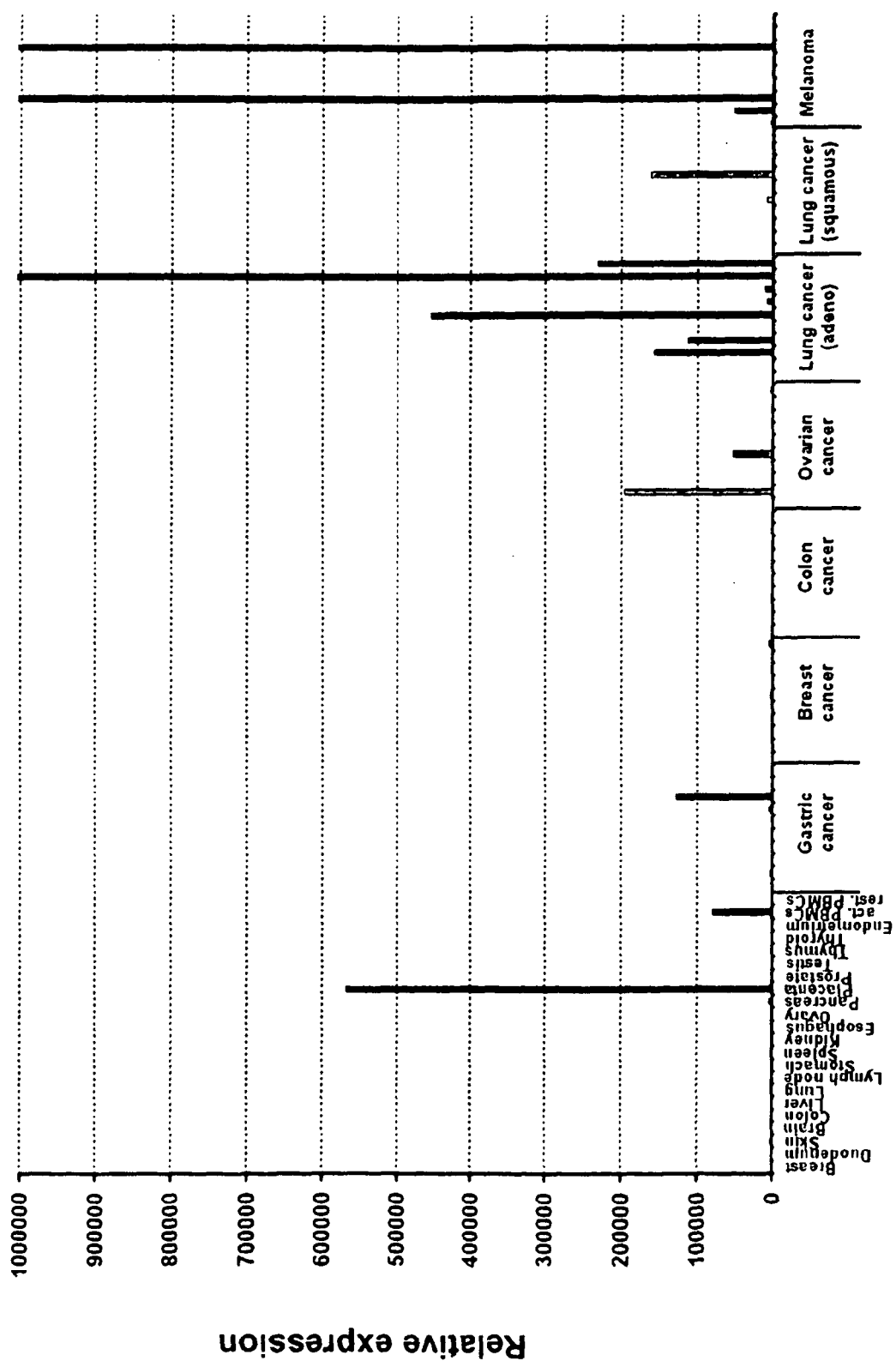


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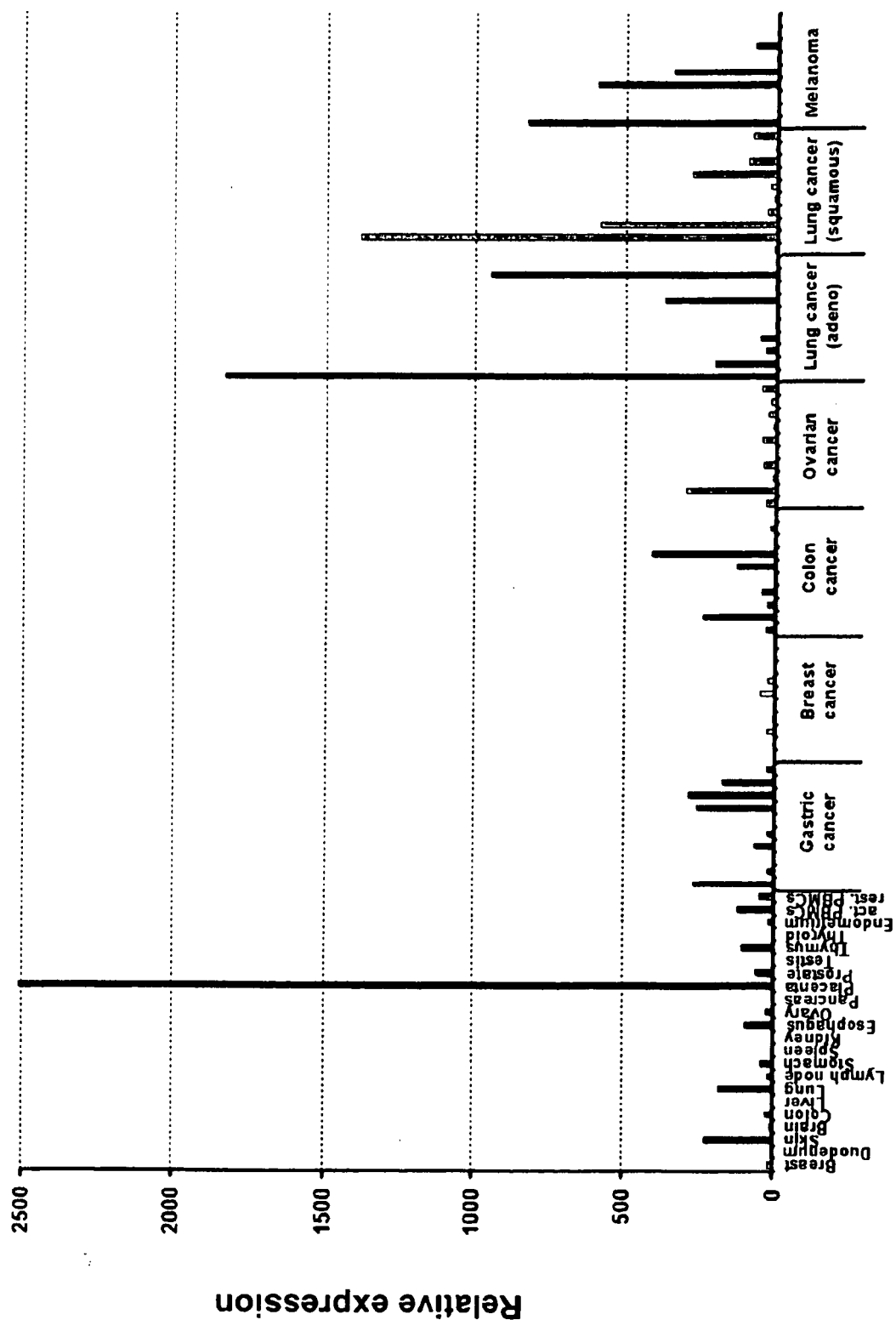


Fig. 15

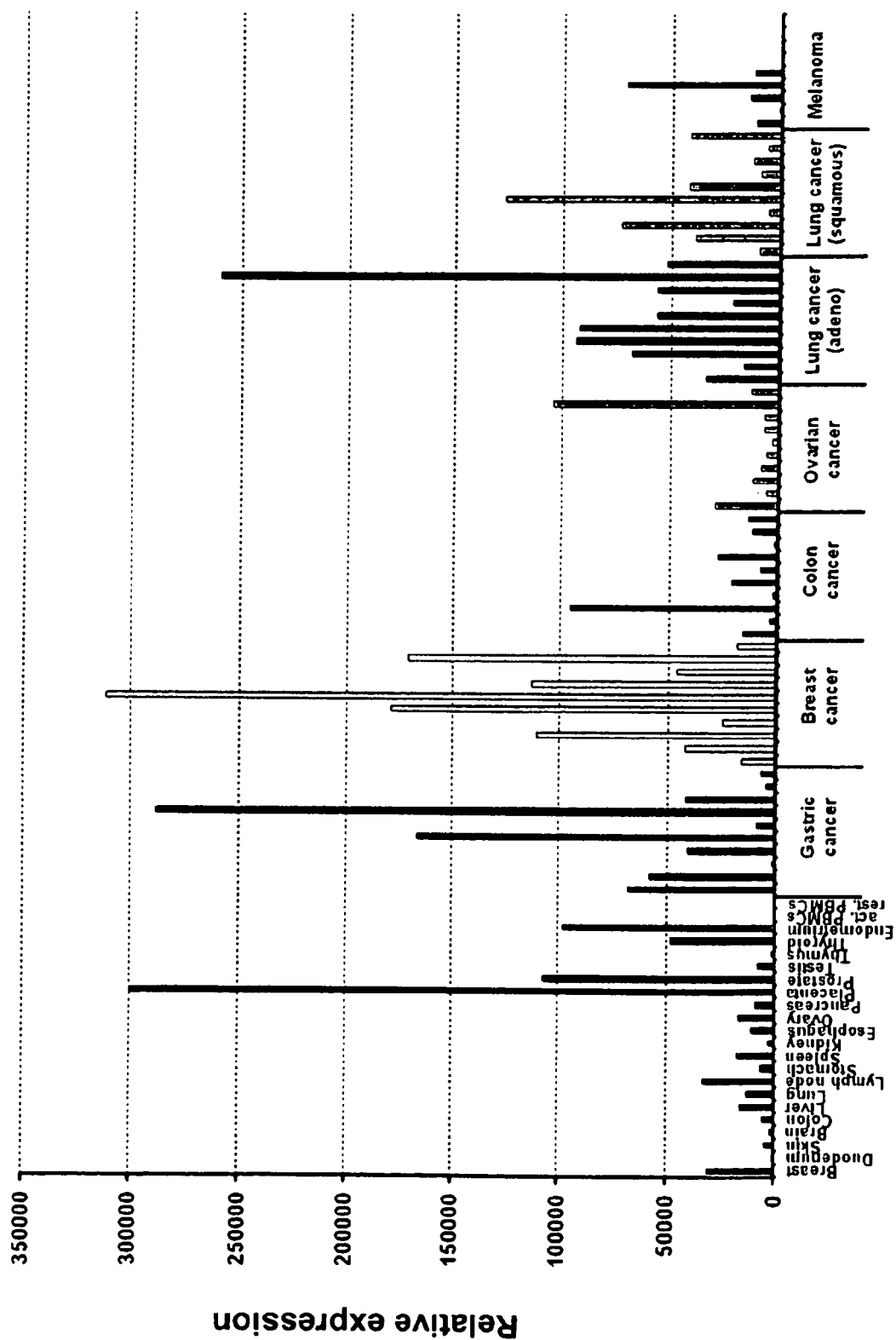


Fig. 16

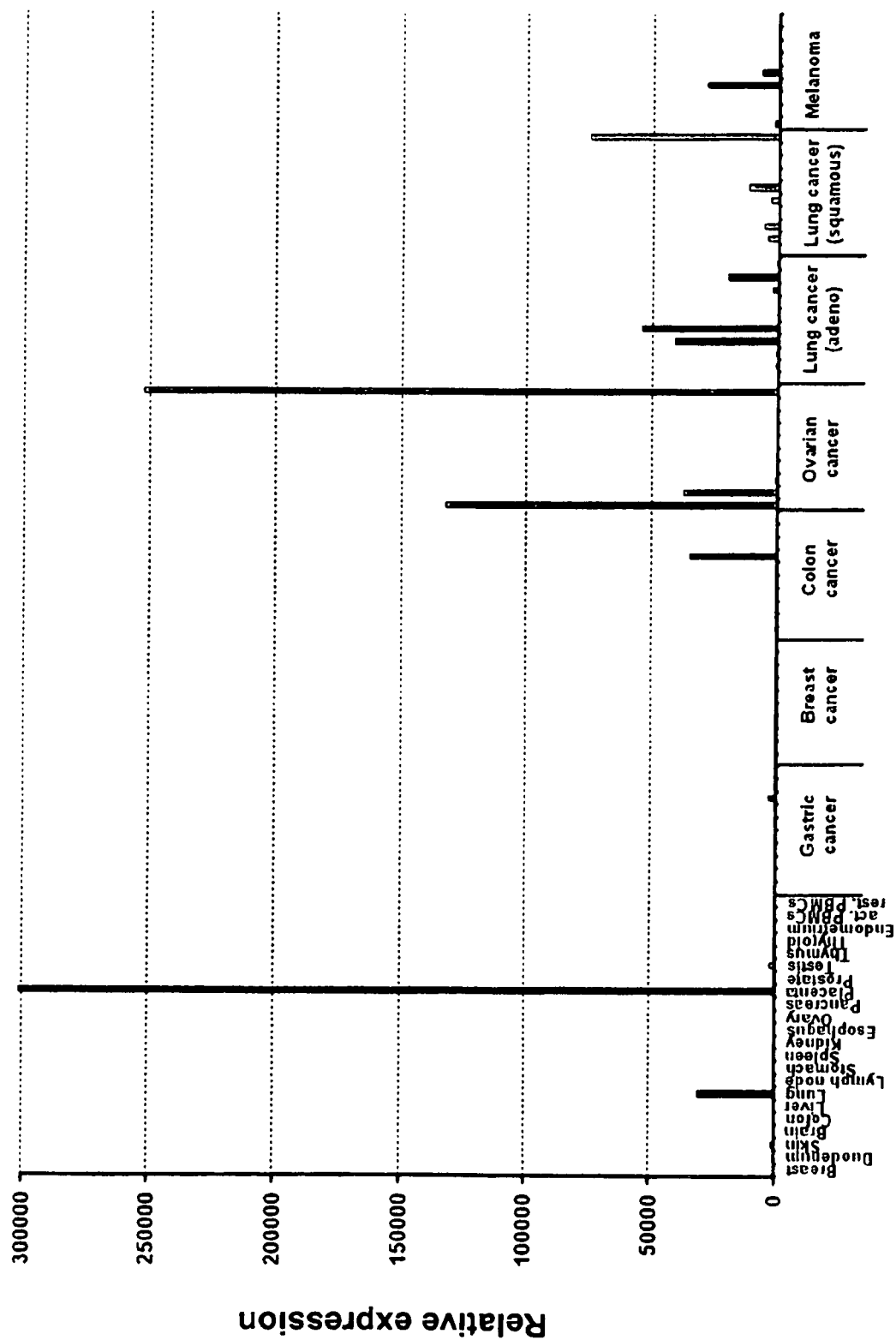


Fig. 17

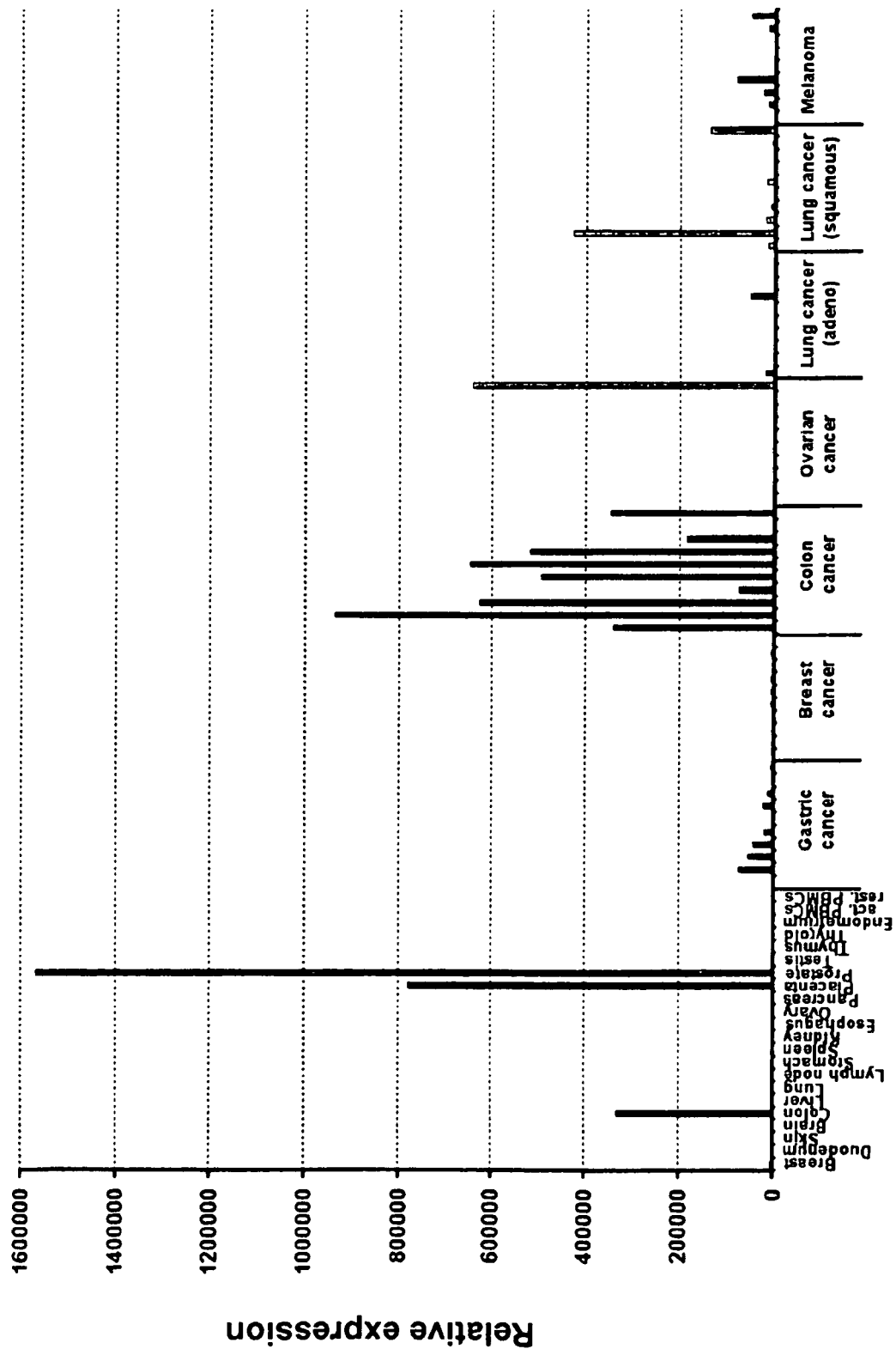


Fig. 18

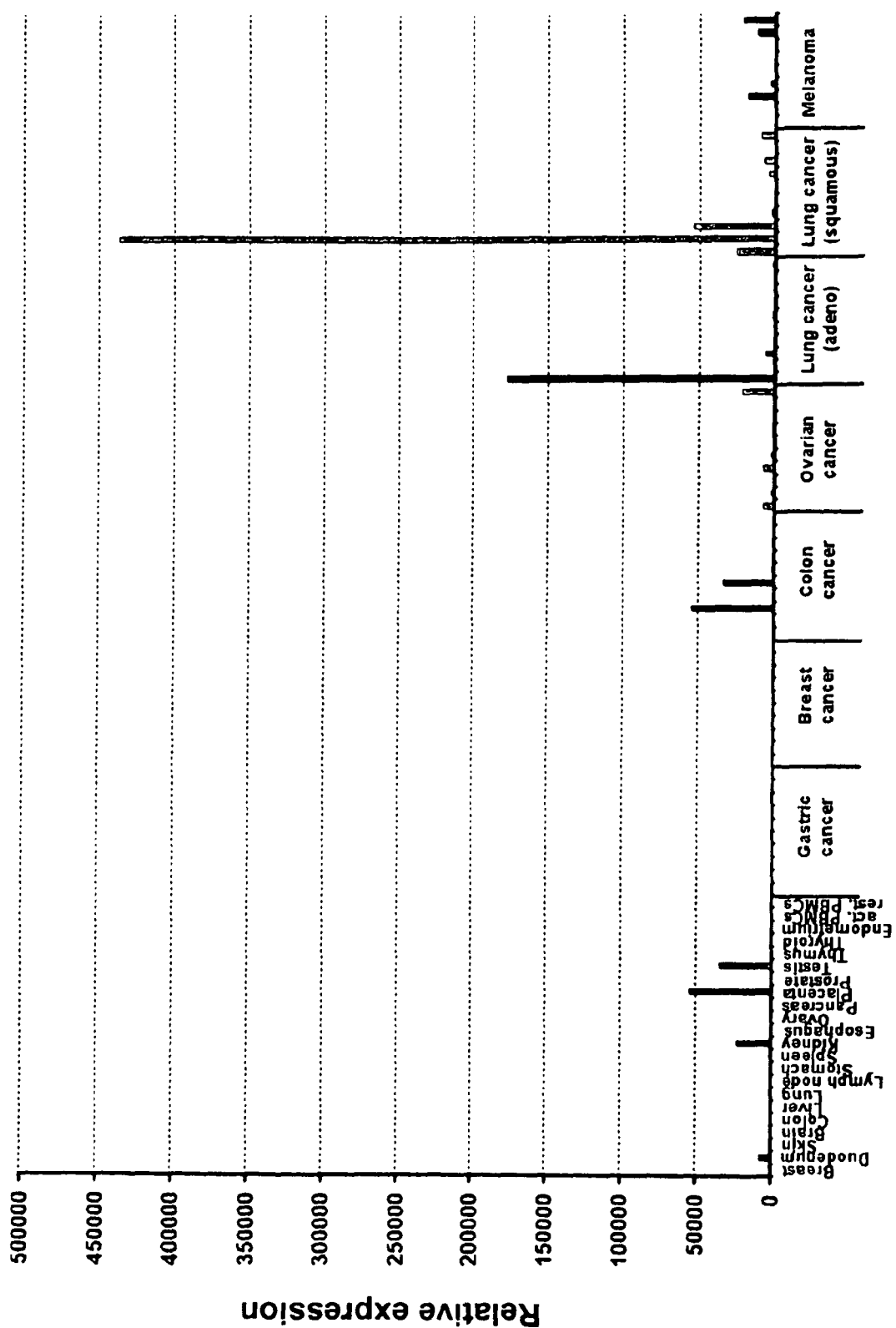


Fig. 19

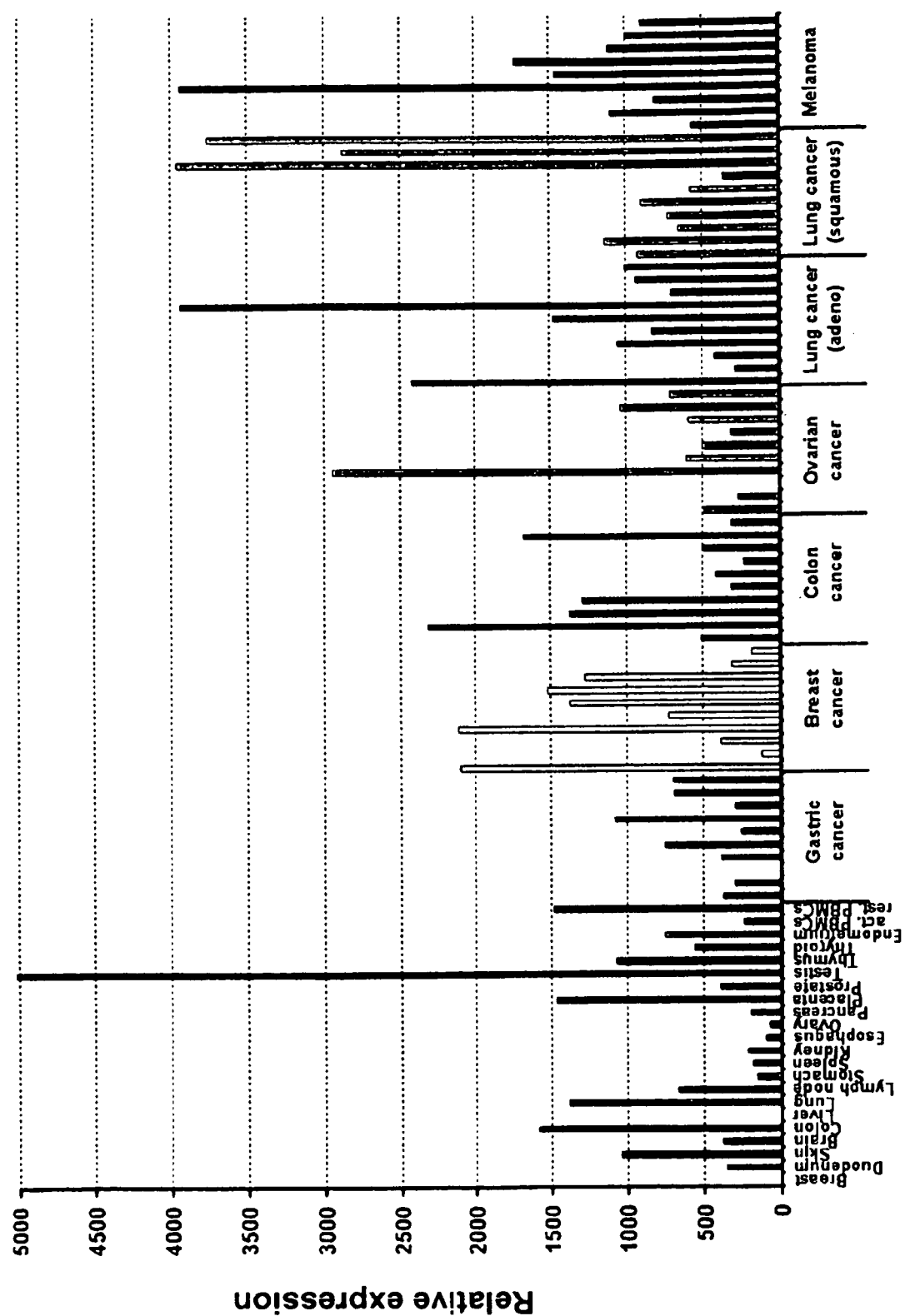


Fig. 20

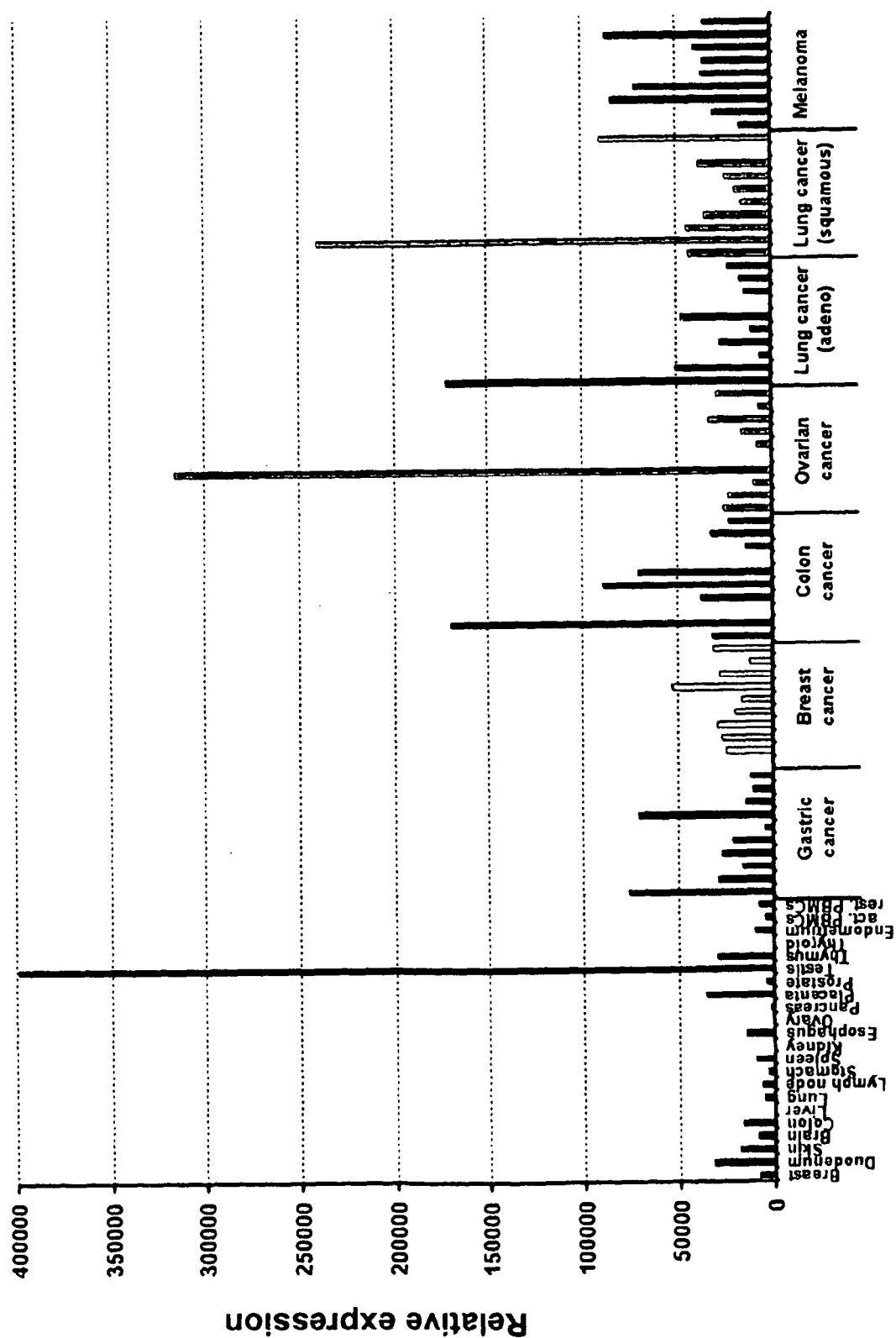


Fig. 21

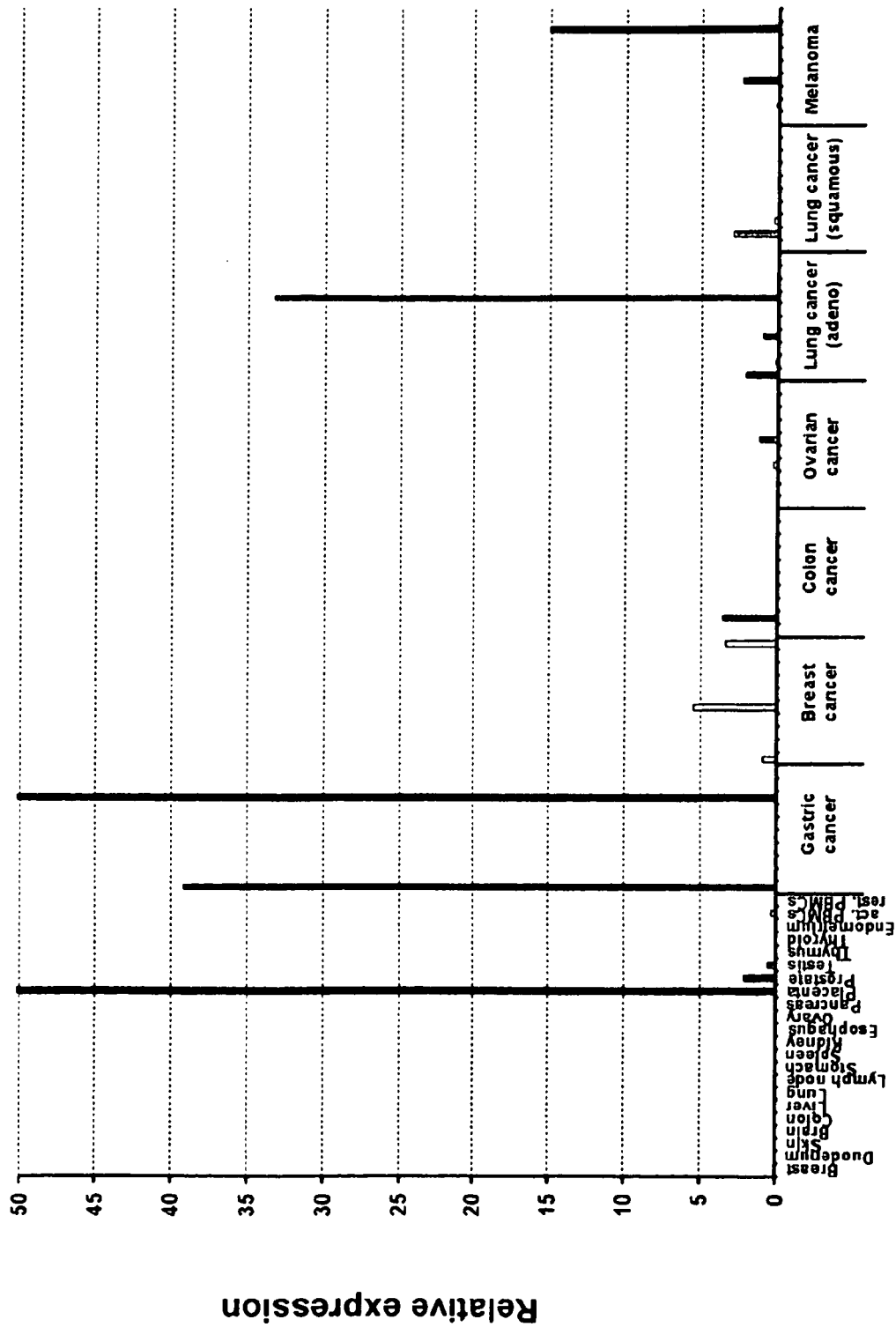


Fig. 22

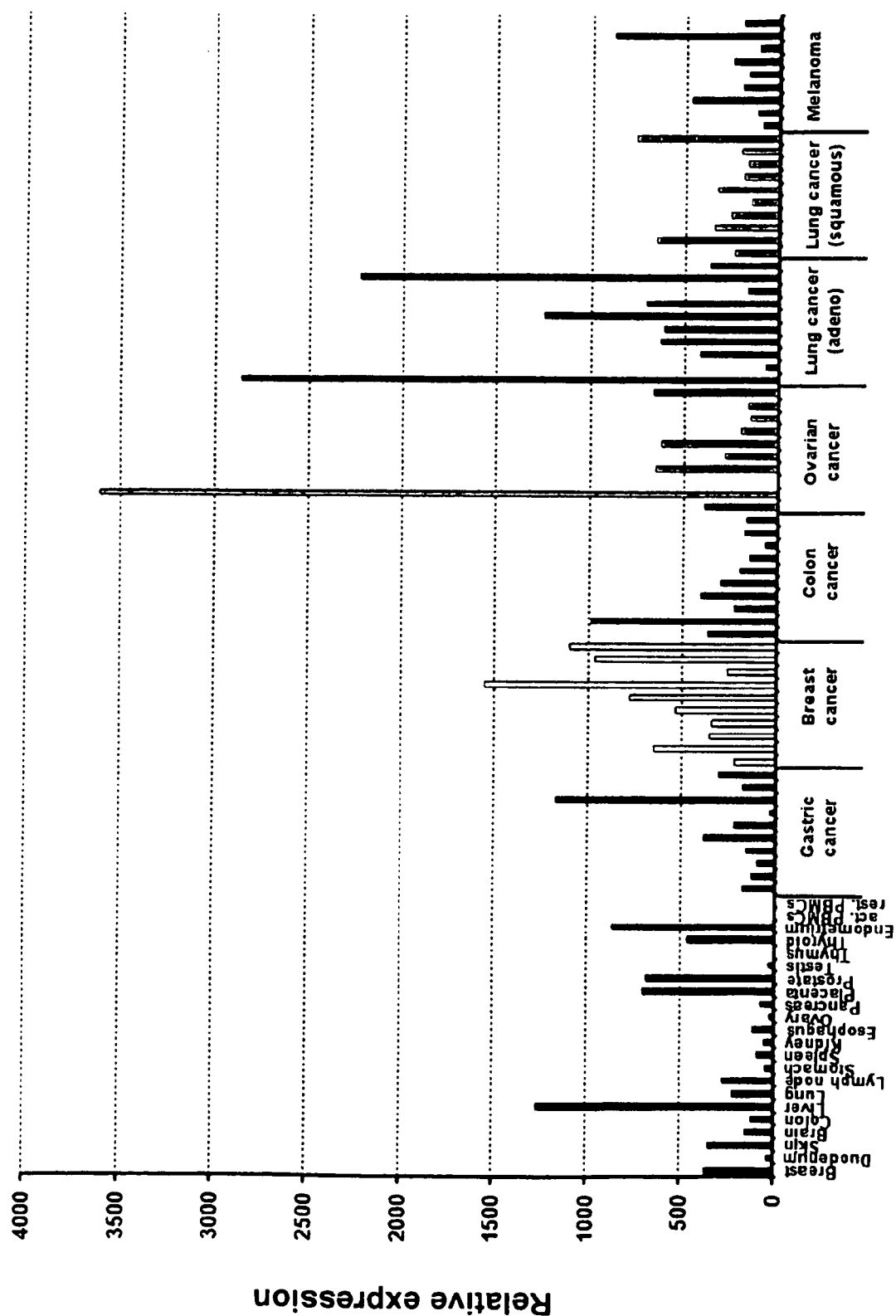


Fig. 23

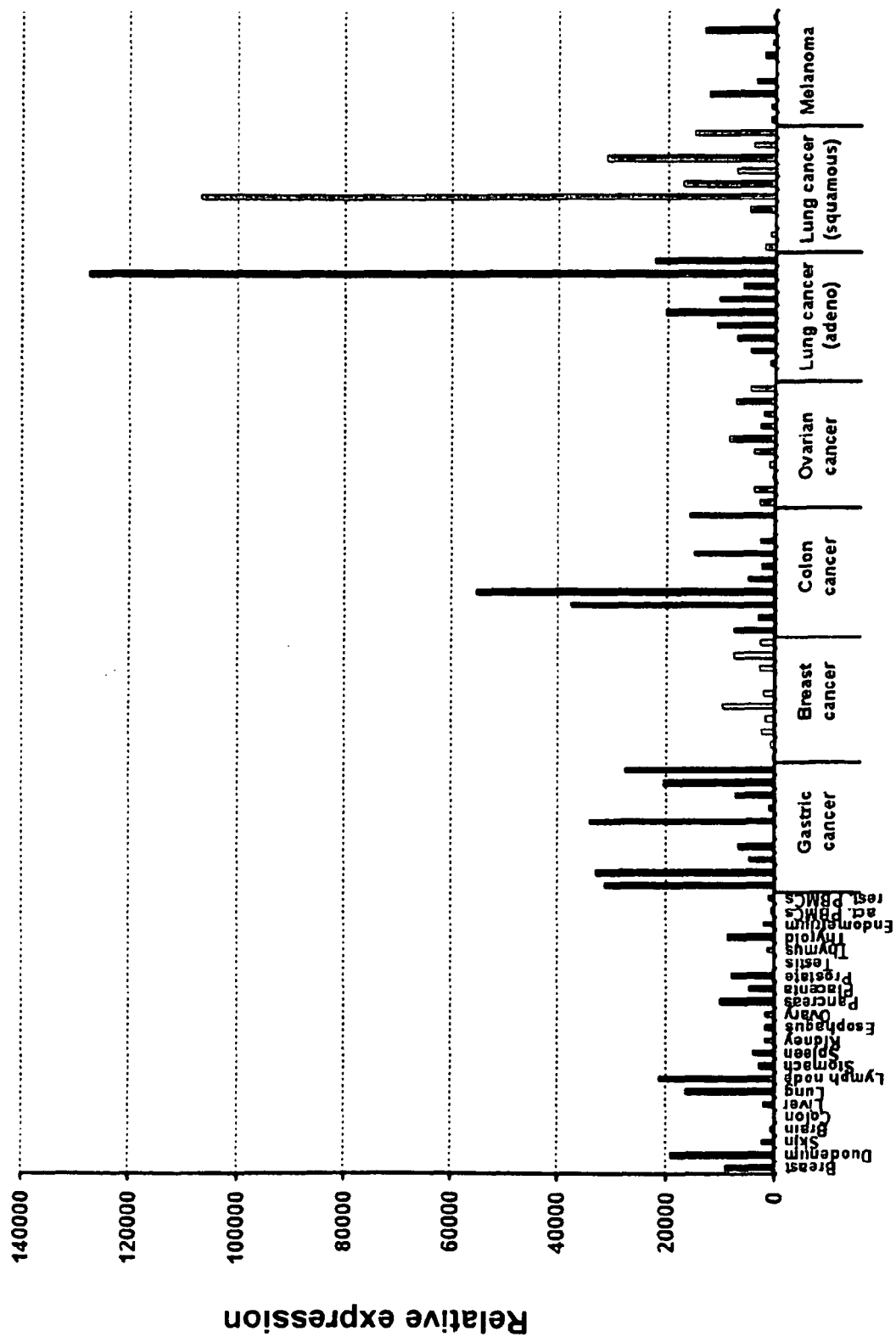


Fig. 24

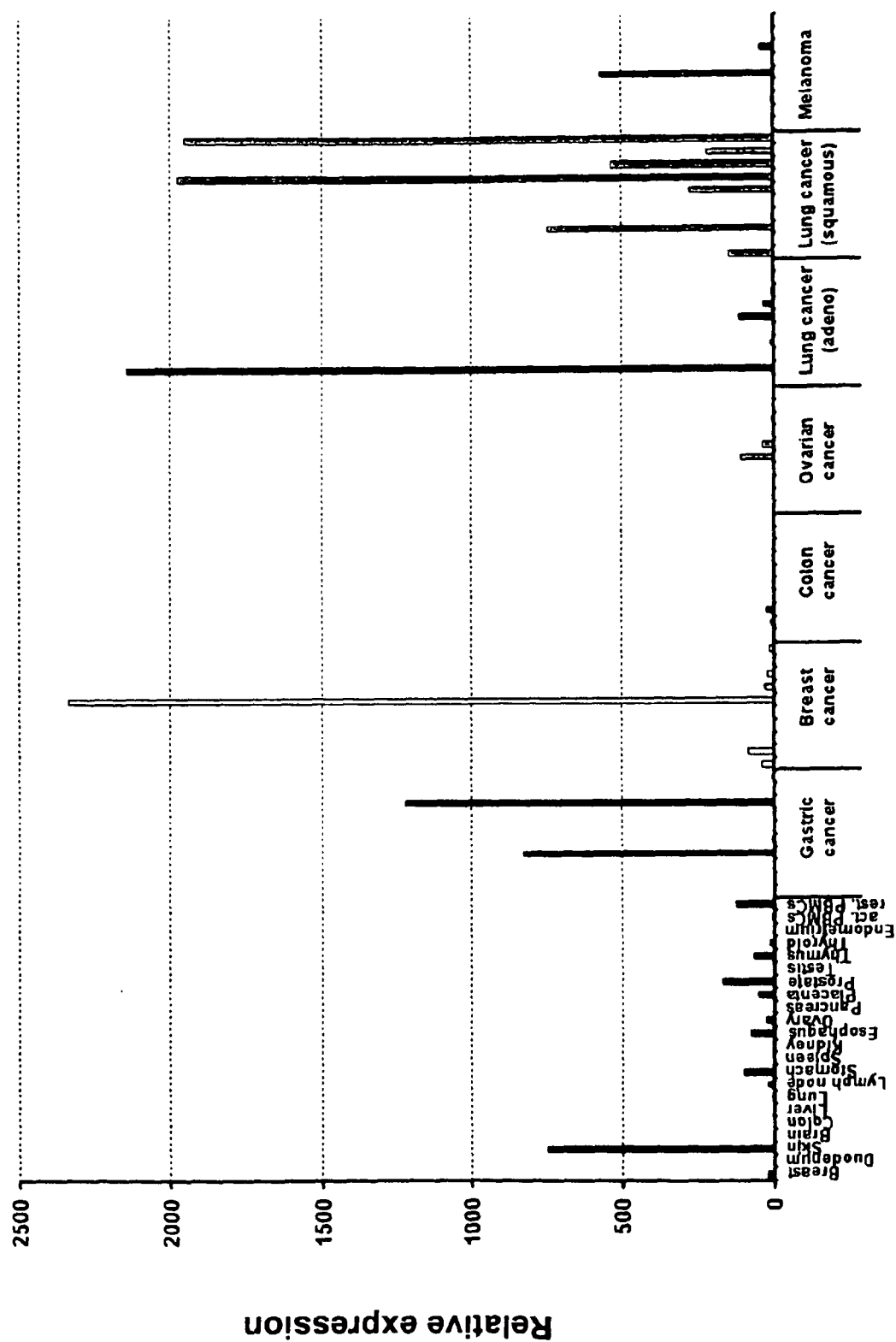


Fig. 25

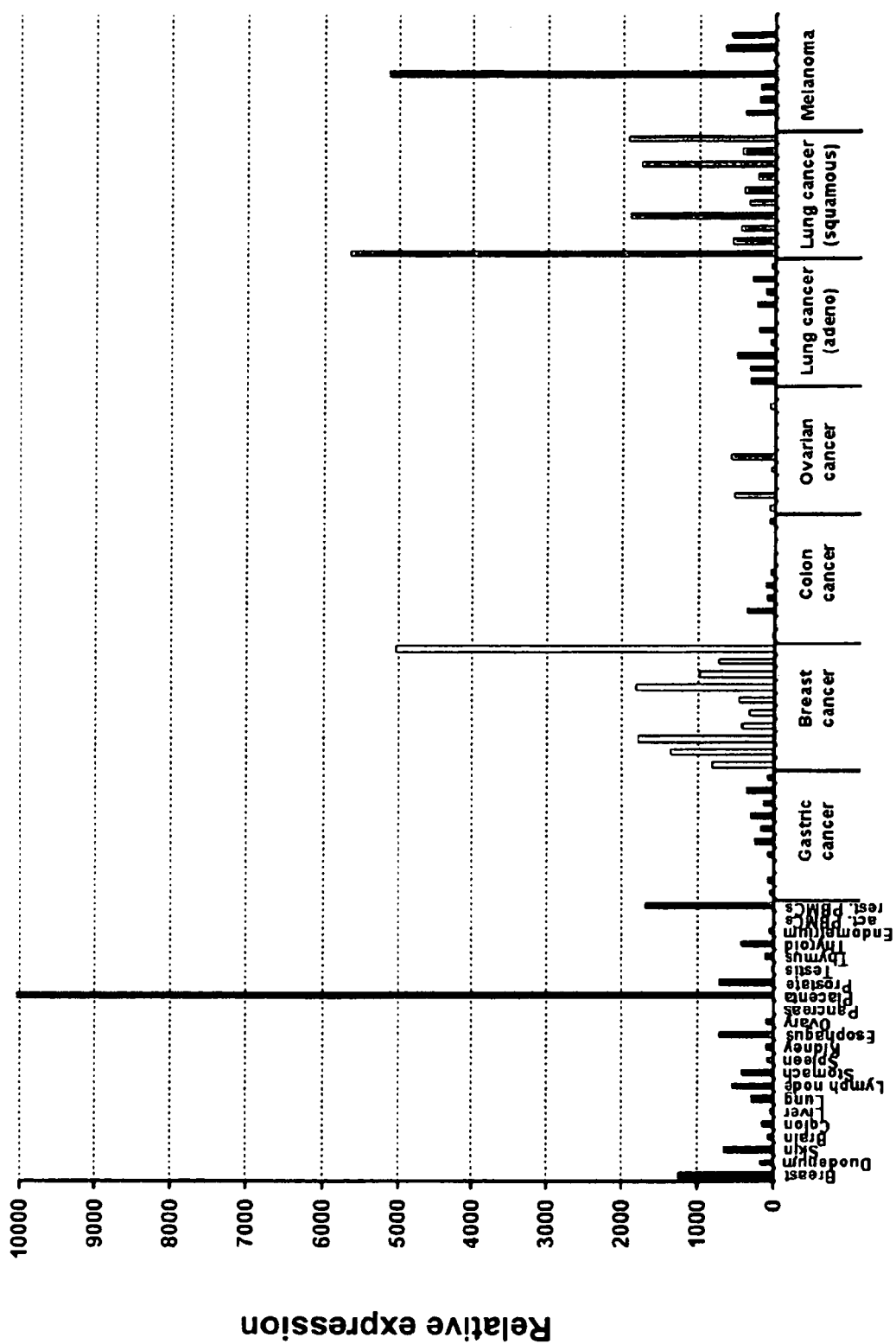
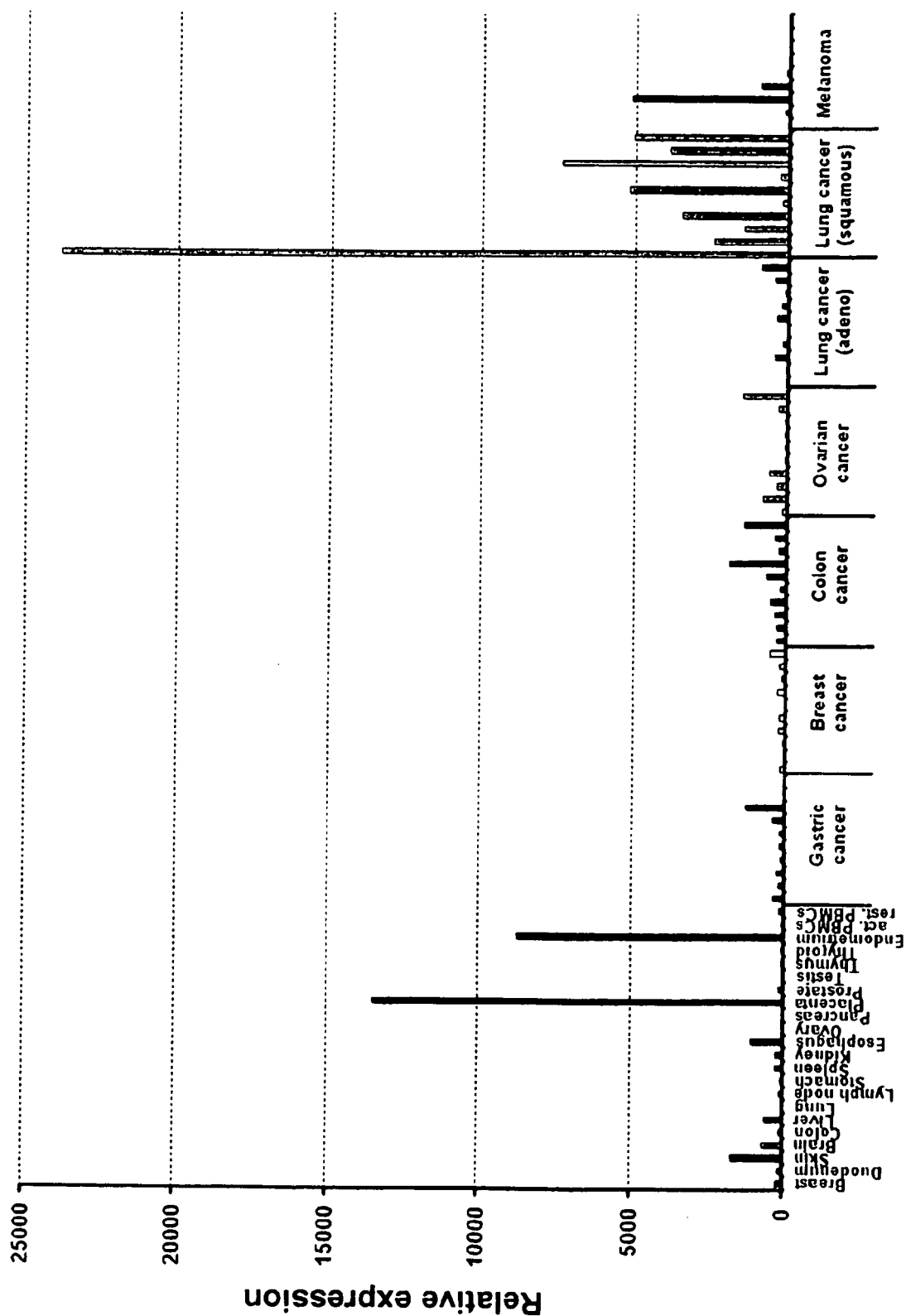


Fig. 26



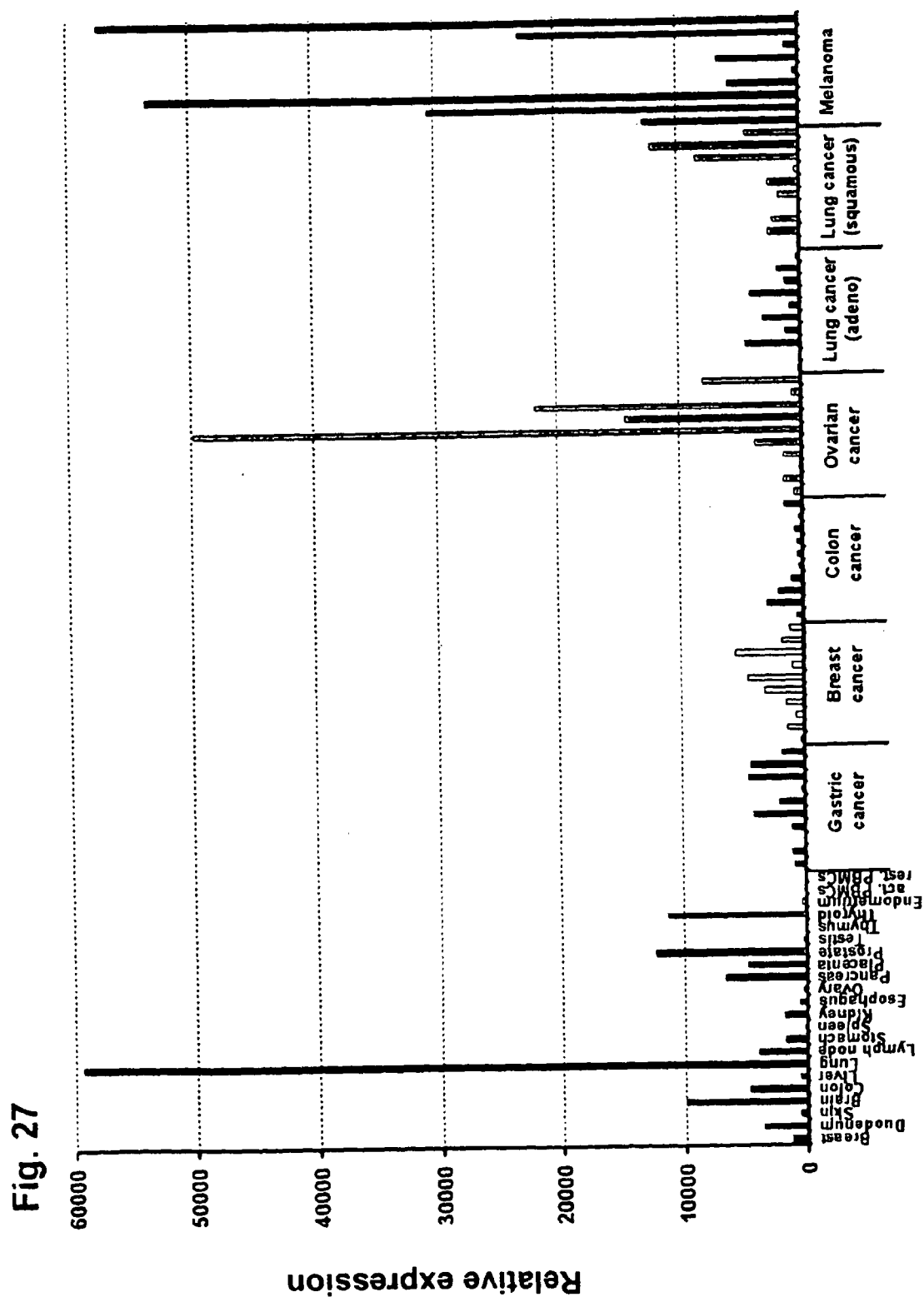
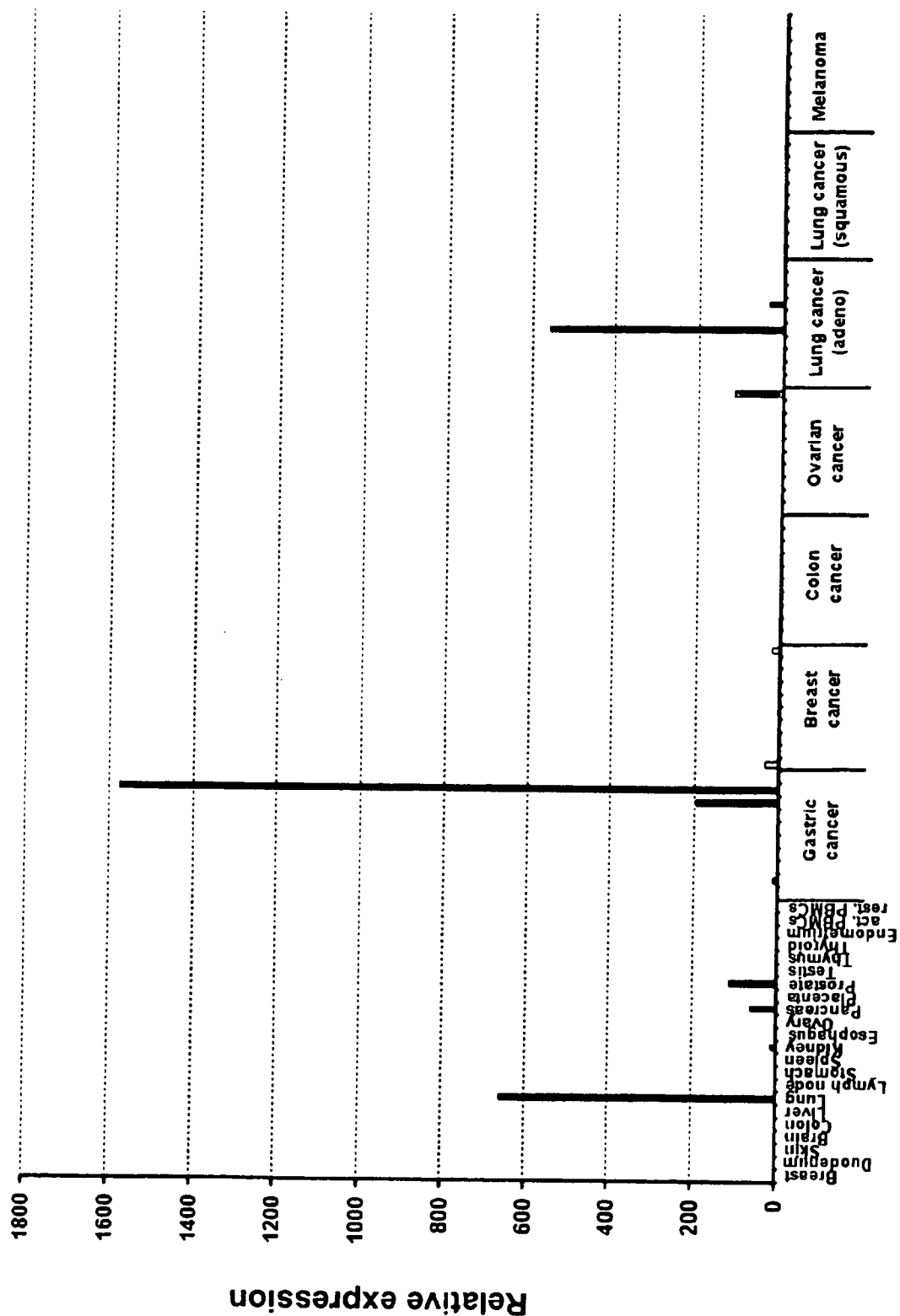


Fig. 28



REFERENCES CITED IN THE DESCRIPTION

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